M K L Q C V S L W 9
GAATTCCGACAAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC ATG AAG TTA CAG TGT GTT TCC CTT TGG 69

L L G T I L I L C S V D N H G L R R C L 29
CTC CTG GGT ACA ATA CTG ATA TTG TGC TCA GTA GAC AAC CAC GGT CTC AGG AGA TGT CTG 129

I S T D M H H I E E S F Q E I K R A I Q 49
ATT TCC ACA GAC ATG CAC CAT ATA GAA GAG AGT TTC CAA GAA ATC AAA AGA GCC ATC CAA 189

A K D T F P N V T I L S T L E T L Q I I 69
GCT AAG GAC ACC TTC CCA AAT GTC ACT ATC CTG TCC ACA TTG GAG ACT CTG CAG ATC ATT 249

K P L D V C C V T K N L L A F Y V D R V 89
AAG CCC TTA GAT GTG TGC TGC GTG ACC AAG AAC CTC CTG GCG TTC TAC GTG GAC AGG GTG 309

F K D H Q E P N P K I L R K I S S I A N 109
TTC AAG GAT CAT CAG GAG CCA AAC CCC AAA ATC TTG AGA AAA ATC AGC AGC ATT GCC AAC 369

S F L Y M Q K T L R Q C Q E Q R Q C H C 129
TCT TTC CTC TAC ATG CAG AAA ACT CTG CGG CAA TGT CAG GAA CAG AGG CAG TGT CAC TGC 429

R Q E A T N A T R V I H D N Y D Q L E V 149
AGG CAG GAA GCC ACC AAT GCC ACC AGA GTC ATC CAT GAC AAC TAT GAT CAG CTG GAG GTC 489

H A A A I K S L G E L D V F L A W I N K 169
CAC GCT GCT GCC ATT AAA TCC CTG GGA GAG CTC GAC GTC TTT CTA GCC TGG ATT AAT AAG 549

N H E V M S S A * 178
AAT CAT GAA GTA ATG TCC TCA GCT TGA 576

TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACTGTGGGAGACAGCCCACCTTGAAGGG 655

GAAGGAGATGGGGAAGGCCCCTTGCAGCTGAAAGTCCCACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGC 734

CAAAAAGTCTACTGTGGTATTTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGC 813

CTTCCCATCTAATTTATTGTGAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTGTAGTACACATTGT 892

ACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGAAAAAAAAAAAAAAAAAAAAAAAACCAGCTGAGCGCCGG 971

TCGCTACCAAAGCCGAATTC 991

FIG. 1

```
             1                                                    50
il10-human   ~MHSSALLCC LVLLTGVRAS PGQGTQSENS CTHFPGNLPN MLRDLRDAFS
il10-mouse   ~MPGSALLCC LLLLTGMRIS RGQYSREDNN CTHFPVGQSH MLLELRTAFS
il10-viral   ~MFRASLLCC LVLLAGVWAD NKYDSESGDD CPTLPTSLPH MLHELRAAFS
mda7-mouse   MSWGLQILPC LSLILLLWNQ VPGLEGQEFR FGSCQV.TGV VLPELWEAFW
mda7-human   ~~MQMVVLPC LGFTLLLWSQ VSGAQGQEFH FGPCQV.KGV VPQKLWEAFW
     italy   ~~~~~MKLQC VSLWLL..GT ILILCSVDNH GLRRCL.IST DMHHIEESFQ
 Consensus   -M-GSALLQC L-LLL--WA- VG-LSG-ENH C-H-PV-L-- MLHELREAFS

             51                                                  100
il10-human   RVKTFFQMKD QLDN..LLLK ESLLEDFKGY LGCQALSEMI QFYLEEVMPQ
il10-mouse   QVKTFFQTKD QLDN..ILLT DSLMQDFKGY LGCQALSEMI QFYLVEVMPQ
il10-viral   RVKTFFQMKD QLDN..MLLD GSLLEDFKGY LGCQALSEMI QFYLEEVMPQ
mda7-mouse   TVKNTVQTQD DITSIRLLKP .QVLRNVSGA ESCYLAHSLL KFYLNTVFKN
mda7-human   AVKDTMQAQD NITSARLLQQ .EVLQNVSDA ESCYLVHTLL EFYLKTVFKN
     italy   EIKRAIQAKD TFPNVTILST LETLQIIKPL DVCCVTKNLL AFYVDRVFKD
 Consensus   RVKTFFQ-KD QLDN-RLLLT -SLLQDFKGY LGCQALSE-- QFYLEEV--Q

             101                                                 150
il10-human   AENQDPD..I KAHVNSLGEN LKTLRLRLRR CHRFLPCENK SKAVEQ...V
il10-mouse   AEKHGPE..I KEHLNSLGEK LKTLRMRLRR CHRFLKCENK SKAVEQ...V
il10-viral   AENHSTD.QE KDKVNSLGEK LKTLRVRLRR CHRFLPCENK SKAVEQ...V
mda7-mouse   YHSKIAKFKV LRSFSTLANN FIVIMSQLQP SKDNSMLPIS ESAHQRFLLF
mda7-human   YHNRTVEVRT LKSFSTLANN FVLIVSQLQP SQENEMFSIR DSAHRRFLLF
     italy   HQE..PNPKI LRKISSIANS FLYMQKTLRQ CQEQRQCHCR QEATNATRVI
 Consensus   AENH-P--KI -R---SL--N -KTLRSRLRR CHRFL-CENK SKAVEQFLLV

             151                                  187
il10-human   KNAFNKLQ.E KGIYKAMSEF DIFINYIEAY MTMKIRN
il10-mouse   KSDFNKLE.D QGVYKAMNEF DIFINCIEAY MMIKMKS
il10-viral   KSAFSKLQ.E KGVYKAMSEF DIFINYIEAY MTTKMKN
mda7-mouse   RRTFKQLDTE VALVKAFGEV DILLTWMQKF YHL~~~~
mda7-human   RRAFKQLDVE AALTKALGEV DILLTWMQKF YKL~~~~
     italy   HDNYDQLEVH AAAIKSLGEL DVFLAWINKN HEVMSSA
 Consensus   K-AF--L-VE ---YKAMGEF DIF-NWIE-Y MTLKMKN
```

FIG. 2

cgtccgccac gcgtccggac tagttctaga tcgcgagcgg ccgccctttt tttttttttt 60

ttggaagtcc taggactgat ctccaggacc agcactcttc tcccagccct tagggtcctg 120

ctcggccaag gccttccctg cc atg cga cct gtc agt gtc tgg cag tgg agc 172

ccc tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct 220

ccg tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt 268

cgg ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg 316

gag ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc 364

acg ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag 412

gcc aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc 460

atc tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act 508

gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag 556

gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac 604

tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga 652

att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag 700

ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac 748

aaa ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc 796

ttc ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc 844

caa cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc 892

acg gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat 940

gac acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg 988

cca ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag 1036

tcg aag cct cag ggg gag gcc cgt gtc cgt cta aag ggc ggc gcc cac 1084

cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca 1132

gtc tgt gac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg 1180

gag ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg 1228

ggg cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga 1276

FIG. 3A

cag gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag 1324

gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac 1372

act ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat 1420

gag ggg cga gtc gag gtg caa ata ggg gga cct ggg ccc ctt cgc tgg 1468

ggc ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc 1516

tgt agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc 1564

tgg tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg 1612

cgc tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc 1660

acc cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc 1708

atc tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg 1756

cag gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt 1804

gct gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg 1852

ccc tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac 1900

ctg gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg 1948

tgg cac gag tgc cat ggg cat tac cac agc atg gac atc ttc act cac 1996

tat gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa 2044

gct agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag 2092

cgg tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc 2140

tgg gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg 2188

gat gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac 2236

ttt gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac 2284

tgc aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt 2332

gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc 2380

cag acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac 2431

tggcccctaa tggcaggggt ctgaggctgc cattacctca ggagcttacc aagaaaccca 2491

tgtcagcaac cgcactcatc agaccatgca ctatggatgt ggaactgtca agcagaagtt 2551

FIG. 3B

ttcaccctcc ttcagaggcc agctgtcagt atctgtagcc aagcatggga atctttgctc 2611

ccaggcccag caccgagcag aacagaccag agcccaccac accacaaaga gcagcacctg 2671

actaactgcc cacaaaagat ggcagcagct cattttcttt aataggaggt caggatggtc 2731

agctccagta tctcccctaa gtttaggggg atacagcttt acctctagcc ttttggtggg 2791

ggaaaagatc cagccctccc acctcatttt ttactataat atgttgctag gtataatttt 2851

attttatata aaaagtgttt ctgtgattct tcagaaaaaa aaaaaaaaaa aaaaaaaaaa 2911

aaaaaaaaa 2920

FIG. 3C

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
1   5   10   15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
            20   25   30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
        35   40   45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
    50   55   60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65   70   75   80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
                85   90   95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
            100   105   110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
        115   120   125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
    130   135   140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145   150   155   160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
                165   170   175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
            180   185   190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
        195   200   205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
    210   215   220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225   230   235   240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
                245   250   255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
            260   265   270

FIG. 4A

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val
420 425 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp
435 440 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu
450 455 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
465 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala
515 520 525

Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
530 535 540

FIG. 4B

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys
545 550 555 560

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
565 570 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe
580 585 590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
595 600 605

His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro
610 615 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu
625 630 635 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn
645 650 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His
660 665 670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
705 710 715 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
725 730 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile
740 745 750

Ile
753

FIG. 4C

atgcgacctg tcagtgtctg gcagtggagc ccctggggc tgctgctgtg cctgctgtgc 60

agttcgtgct tggggtctcc gtccccttcc acgggccctg agaagaaggc cgggagccag 120

gggcttcggt tccggctggc tggcttcccc aggaagccct acgagggccg cgtggagata 180

cagcgagctg gtgaatgggg caccatctgc gatgatgact tcacgctgca ggctgcccac 240

atcctctgcc gggagctggg cttcacagag gccacaggct ggacccacag tgccaaatat 300

ggccctggaa caggccgcat ctggctggac aacttgagct gcagtgggac cgagcagagt 360

gtgactgaat gtgcctcccg gggctggggg aacagtgact gtacgcacga tgaggatgct 420

ggggtcatct gcaaagacca gcgcctccct ggcttctcgg actccaatgt cattgaggta 480

gagcatcacc tgcaagtgga ggaggtgcga attcgacccg ccgttgggtg gggcagacga 540

cccctgcccg tgacggaggg gctggtggaa gtcaggcttc ctgacggctg gtcgcaagtg 600

tgcgacaaag gctggagcgc ccacaacagc cacgtggtct gcgggatgct gggcttcccc 660

agcgaaaaga gggtcaacgc ggccttctac aggctgctag cccaacggca gcaacactcc 720

tttggtctgc atggggtggc gtgcgtgggc acggaggccc acctctccct ctgttccctg 780

gagttctatc gtgccaatga caccgccagg tgccctgggg ggggccctgc agtggtgagc 840

tgtgtgccag gccctgtcta cgcggcatcc agtggccaga agaagcaaca acagtcgaag 900

cctcaggggg aggcccgtgt ccgtctaaag ggcggcgccc accctggaga gggccgggta 960

gaagtcctga aggccagcac atggggcaca gtctgtgacc gcaagtggga cctgcatgca 1020

gccagcgtgg tgtgtcggga gctgggcttc gggagtgctc gagaagctct gagtggcgct 1080

cgcatggggc agggcatggg tgctatccac ctgagtgaag ttcgctgctc tggacaggag 1140

ctctccctct ggaagtgccc ccacaagaac atcacagctg aggattgttc acatagccag 1200

gatgccgggg tccggtgcaa cctaccttac actggggcag agaccaggat ccgactcagt 1260

ggggggccgca gccaacatga ggggcgagtc gaggtgcaaa taggggggacc tgggcccctt 1320

cgctggggcc tcatctgtgg ggatgactgg gggaccctgg aggccatggt ggcctgtagg 1380

caactgggtc tgggctacgc caaccacggc ctgcaggaga cctggtactg ggactctggg 1440

aatataacag aggtggtgat gagtggagtg cgctgcacag ggactgagct gtccctggat 1500

FIG. 5A

```
cagtgtgccc atcatggcac ccacatcacc tgcaagagga cagggacccg cttcactgct 1560
ggagtcatct gttctgagac tgcatcagat ctgttgctgc actcagcact ggtgcaggag 1620
accgcctaca tcgaagaccg gcccctgcat atgttgtact gtgctgcgga agagaactgc 1680
ctggccagct cagcccgctc agccaactgg ccctatggtc accggcgtct gctccgattc 1740
tcctcccaga tccacaacct gggacgagct gacttcaggc ccaaggctgg gcgccactcc 1800
tgggtgtggc acgagtgcca tgggcattac cacagcatgg acatcttcac tcactatgat 1860
atcctcaccc caaatggcac caaggtggct gagggccaca aagctagttt ctgtctcgaa 1920
gacactgagt gtcaggagga tgtctccaag cggtatgagt gtgccaactt tggagagcaa 1980
ggcatcactg tgggttgctg ggatctctac cggcatgaca ttgactgtca gtggattgac 2040
atcacggatg tgaagccagg aaactacatt ctccaggttg tcatcaaccc aaactttgaa 2100
gtagcagaga gtgactttac caacaatgca atgaaatgta actgcaaata tgatggacat 2160
agaatctggg tgcacaactg ccacattggt gatgccttca gtgaagaggc caacaggagg 2220
tttgaacgct accctggcca gaccagcaac cagattatc                        2259
```

FIG. 5B

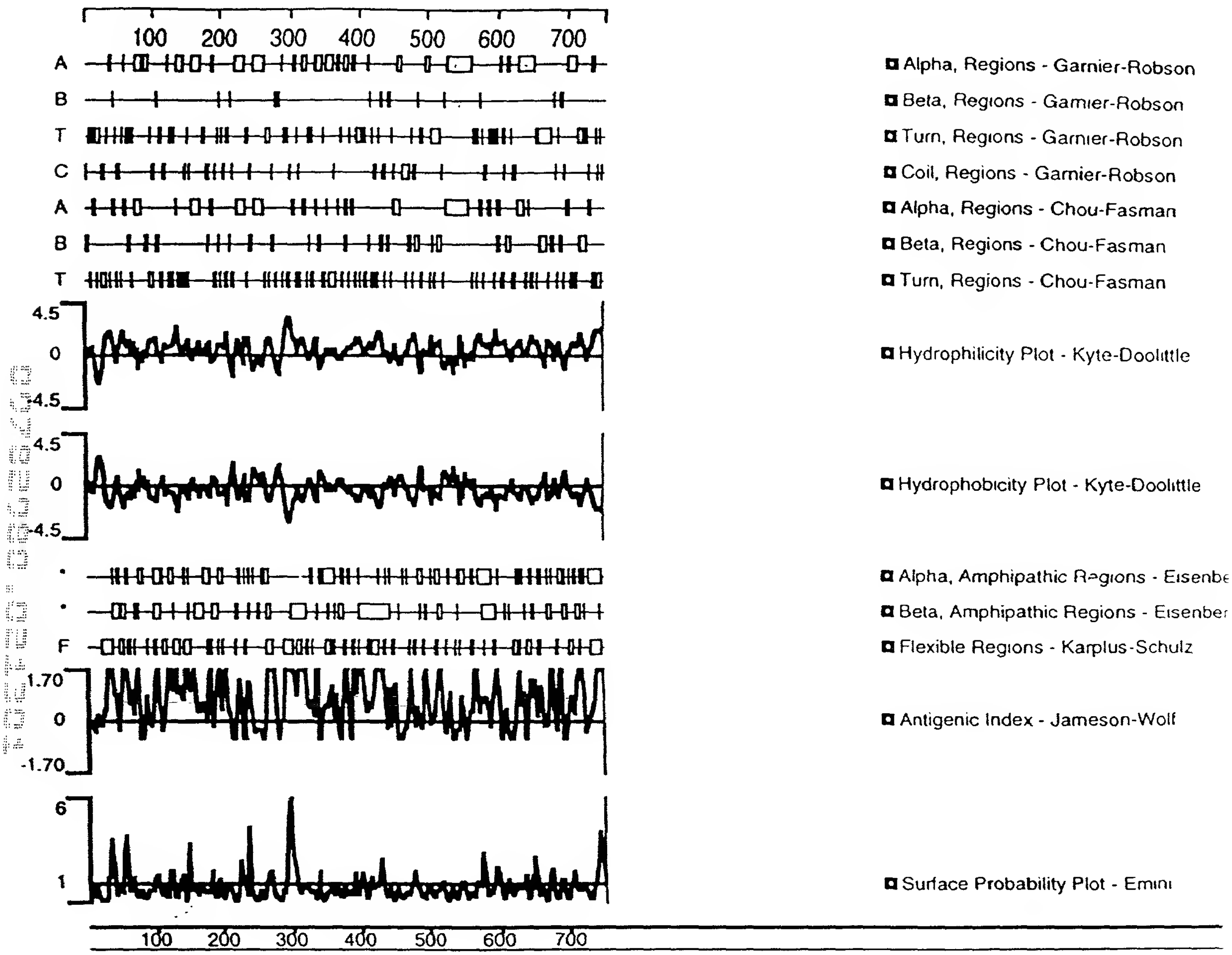

100
200
300
400
500
600
700
A
B
T
C
A
B
T
4.5
0
-4.5
4.5
0
-4.5
F
1.70
0
-1.70
6
1
Alpha, Regions - Garnier-Robson
Beta, Regions - Garnier-Robson
Turn, Regions - Garnier-Robson
Coil, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Chou-Fasman
Turn, Regions - Chou-Fasman
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenbe
Beta, Amphipathic Regions - Eisenber
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

FIG. 6

```
         1                                                          60
LOX      MRFA--------WTVLLLGPLQ-----------LCALVHCAPPAAGQQQP----------
huLOL    MALA--------RGSRQLGALV-------WGACLCVLVH------GQQAQ----------
huLor    MERPLCSHLCSCLAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPQAPANVAKIQLRL
muLor-2  M-RAVSVWYCCPWGLLLLHCL-C----------SFSVGSPSPS-ISPEKKVGSQGLRFRL
huLor-2  M-RPVSVWQWSPWGLLL--CLLC----------SSCLGSPSPS-TGPEKKAGSQGLRFRL

         61                                                        120
LOX      ---PREPPAAPGAWRQQIQWENN-GQVFSL-----LSLGSQY------------------
huLOL    ---P-GQGSDPARWRQLIQWENN-GQVYSL-----LNSGSEYVPA-----GPQRSESSSR
huLor    AGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGP
muLor-2  AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHVLCRELGFTEATGWTHSAKYGPGTGR
huLor-2  AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGR

         121                                                       180
LOX      ------------------------QPQRRRDPGAA-------VPG---AANASAQQPRTP
huLOL    VLLA--------GAPQAQQRRSHGSPRRRQAPSLP-------LPG-RVGSDTVRGQARHP
huLor    IWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLN
muLor-2  IWLDNLSCRGTEGSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-Q
huLor-2  IWLDNLSCSGTEQSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-H

         181                                                       240
LOX      ILL--IRD----N---------------RTAAG------RTRTAGSSGVTAG--------
huLOL    FGFGQVPD----NWREVAVGDSTGMALARTSVS------QQRHGGSASSVSAS-AFAST-
huLor    IQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKNSRVVCGMFGFPGER
muLor-2  LQVEEVRLRPAVEWGRRPLPVTEGLVEVRLPEGWSQVCDKGWSAHNSHVVCGMLGFPGEK
huLor-2  LQVEEVRIRPAVGWGRRPLPVTEGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEK

         241                                                       300
LOX      -------RP-RPTARHWF---------------------QAGY------------STSRA
huLOL    ------YRQ-QPSYPQQFPY------------------PQAPF----VSQYENYDPASRT
huLor    TYNTKVYKMFASRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNVTCENGLPAVVS
muLor-2  RVNMAFYRMLAQKKQHSFGLHSVACVGTEAHLSLCSLE---FYRANDTTRCSGGNPAVVS
huLor-2  RVNAAFYRLLAQRQQHSFGLHGVACVGTEAHLSLCSLE---FYRANDTARCPGGGPAVVS

         301                                                       360
LOX      -------------------REAGPSR----AENQTAPGEVPAL------------SNLRP
huLOL    YDQGFVY-----------YRPAGGGV----GAGAAAVASAGVI------------YPYQP
huLor    CVPGQVFSPDGPSRFRKAYKPE-QPLVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVS
muLor-2  CVLGPLYATFTGQKKQQHSKPQGEARVRLKGGAHQGEGRVEVLKAGTWGTVCDRKWDLQA
huLor-2  CVPGPVYAASSGQKKQQQSKPQGEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHA

         361                                                       420
LOX      PS------------------RVDGMVGDD-------------------PYNP-------
huLOL    RA------------------RYEEYGGGEELPEYPPQG----FYPAPERPYVPPPPPPPD
huLor    ASVVCRELGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNA-ESQGCNHEE
muLor-2  ASVVCPELGFGTAREALSGARMGQGMGAIHLSEVRCSGQEPSLWRCPSKNITAEDCSHSQ
huLor-2  ASVVCRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQ
```

FIG. 7A

```
           421                                                        480
LOX        -----YK---YSDDNPYYNYYDTYERPRPG-----------GRYRP---------GYGTG
huLOL      GLDRRYSHSLYSEGTPGFE--QAYPDPGPEAAQAHGGDPRLGWYPPYANP--PPEAYGPP
huLor      DAGVRCNTP-AMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVC
muLor-2    DAGVRCNLP-YTGVETKIRLSGGRSRYEGRVEVQIGIPGHLRWGLICGDDWGTLEAMVAC
huLor-2    DAGVRCNLP-YTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVAC

           481                                                        540
LOX        ------Y-----------------FQ---------------------------------Y
huLOL      RALEPPY-----------------LPVRSSDTPPPGGE-------RNGAQQGRLSVGSVY
huLor      RQLGLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQY
muLor-2    RQLGLGYANHGLQETWYWDSG-NVTEVVMSGVRCTGSELSLNQCAHHSSHITCKKTGTRF
huLor-2    RQLGLGYANHGLQETWYWDSG-NITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRF

           541                                                        600
LOX        --------GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVL
huLOL      RPNQN-GRGLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVL
huLor      GAGVACSETAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTD-PTTGYRRL
muLor-2    TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL
huLor-2    TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL

           601                                                        660
LOX        LRFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKAS
huLOL      LRFPQRVKNQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKAS
huLor      LRFSSQIHNNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLN-GTKVAEGHKAS
muLor-2    LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS
huLor-2    LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS

           661                                                        720
LOX        FCLEDTSCDYGYHRRFACTAHT-QGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVN
huLOL      FCLEDSTCDFGNLKRYACTSHT-QGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVN
huLor      FCLEDTECEGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVIN
muLor-2    FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN
huLor-2    FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN

           721                                                       779
LOX        PSYLVPESDYTNNVVRCDIRYTGHHAYASGCTI-----------------------SPY
huLOL      PKYIVLESDFTNNVVRCNIHYTGRYVSATNCKI-----------------------VQS
huLor      PNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ
muLor-2    PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQIV--
huLor-2    PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII--
```

FIG. 7B

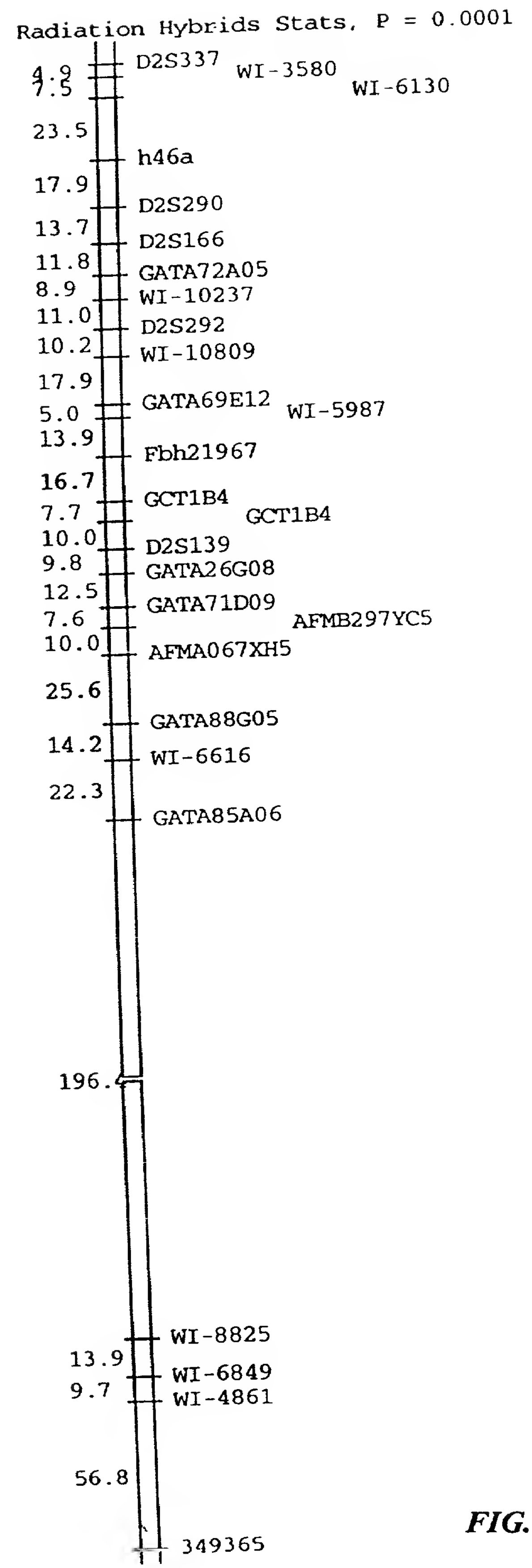
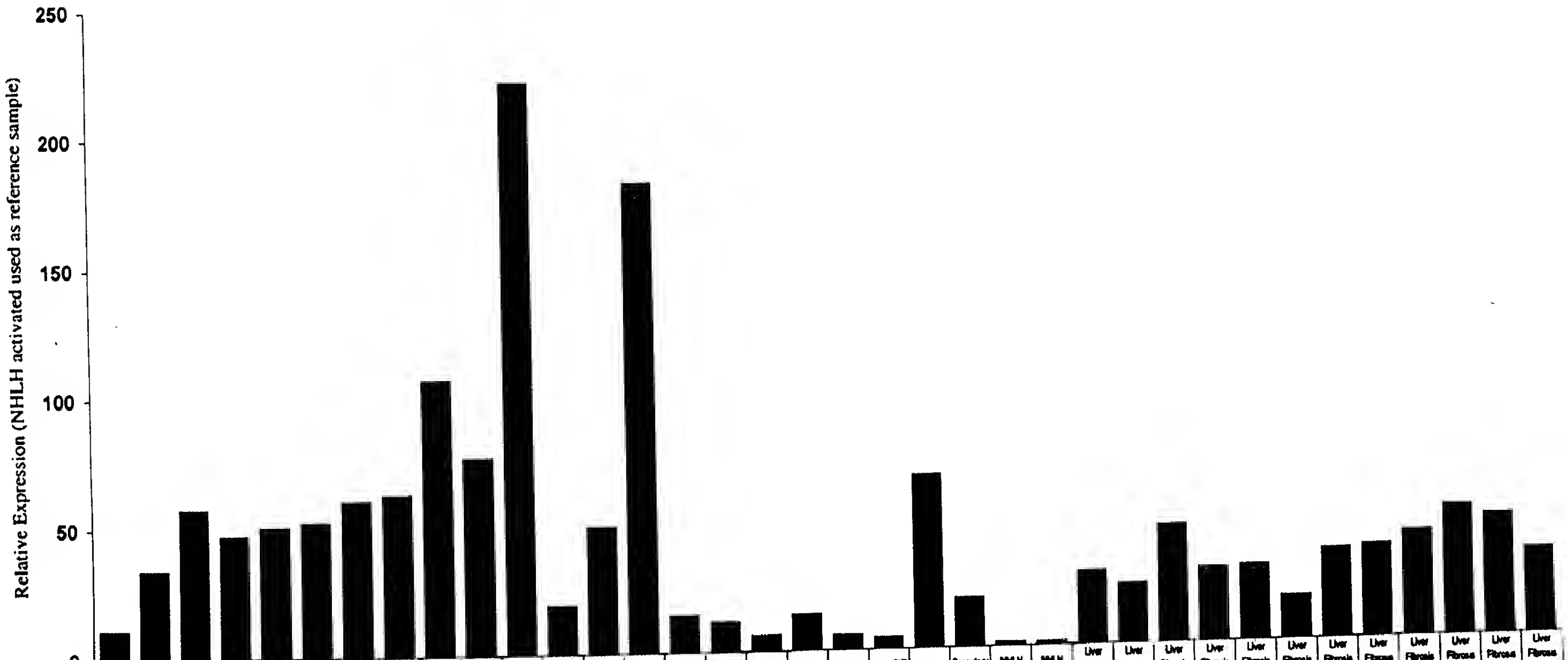

Radiation Hybrids Stats, P = 0.0001
D2S337
WI-3580
WI-6130
4.9
7.5
23.5
h46a
17.9
D2S290
13.7
D2S166
11.8
GATA72A05
8.9
WI-10237
11.0
D2S292
10.2
WI-10809
17.9
GATA69E12
WI-5987
5.0
13.9
Fbh21967
16.7
GCT1B4
7.7
GCT1B4
10.0
D2S139
9.8
GATA26G08
12.5
GATA71D09
7.6
AFMB297YC5
10.0
AFMA067XH5
25.6
GATA88G05
14.2
WI-6616
22.3
GATA85A06
196.
WI-8825
13.9
WI-6849
9.7
WI-4861
56.8
349365

FIG. 8



	Lymph Node (MPI 78)	Lymph Node (NDR 173)	Heart (PIT 272)	Heart (PIT 273)	Lung (MPI 131)	Lung (NDR 189)	Kidney (MPI 58)	Spleen (MPI 380)	SK Muscle (MPI 38)	Fetal Liver (MPI 435)	Fetal Liver (MPI 133)	Tonsil (MPI 37)
21967	30.56	29.93	28.145	29.375	29.86	27.165	30.695	27.005	29.46	30.085	31.57	28.49
Beta 2	14.17	19.19	18.17	19.11	19.48	17.05	20.78	17.15	20.40	20.86	23.49	17.89
Rel. Exp.	10.78	33.59	57.08	46.85	50.04	51.98	60.13	62.25	108.15	75.86	221.32	18.84

	Brain (MPI 463)	Brain (MPI 422)	Liver (MPI 75)	Liver (MPI 385)	Liver(MPI 338)	Liver (NDR 154)	Liver (NDR 208)	Liver (PIT 280)	CD14	Granulocytes	NHLH resting	NHLH activated
21967	30.045	33.685	32.935	31.08	33.865	32	33.75	32.705	26.945	30.825	35.595	35.57
Beta 2	19.83	22.22	20.84	18.77	20.74	19.87	20.37	18.87	17.19	19.24	19.92	19.76
Rel. Exp.	48.50	191.65	14.07	11.35	5.92	13.74	8.41	4.23	65.49	18.77	1.10	1.00

	Liver Fibrosis (MPI 447)	Liver Fibrosis (NDR 190)	Liver Fibrosis (NDR 191)	Liver Fibrosis (NDR 182)	Liver Fibrosis (NDR 183)	Liver Fibrosis (NDR 204)	Liver Fibrosis (NDR 126)	Liver Fibrosis (NDR 116)	Liver Fibrosis (NDR 78)	Liver Fibrosis (NDR 112)	Liver Fibrosis (NDR 225)	Liver Fibrosis (NDR 141)
21967	29.32	35.495	30.105	33.415	30.785	33.36	31.9	29.175	30.87	31.955	30.845	33.045
Beta 2	16.30	24.18	19.77	22.41	19.83	21.58	21.18	18.51	20.39	21.77	20.36	22.25
Rel. Exp.	27.67	43.59	44.93	27.95	28.74	18.34	34.18	35.51	40.22	49.52	45.89	32.45

Tissue Type

FIG. 9

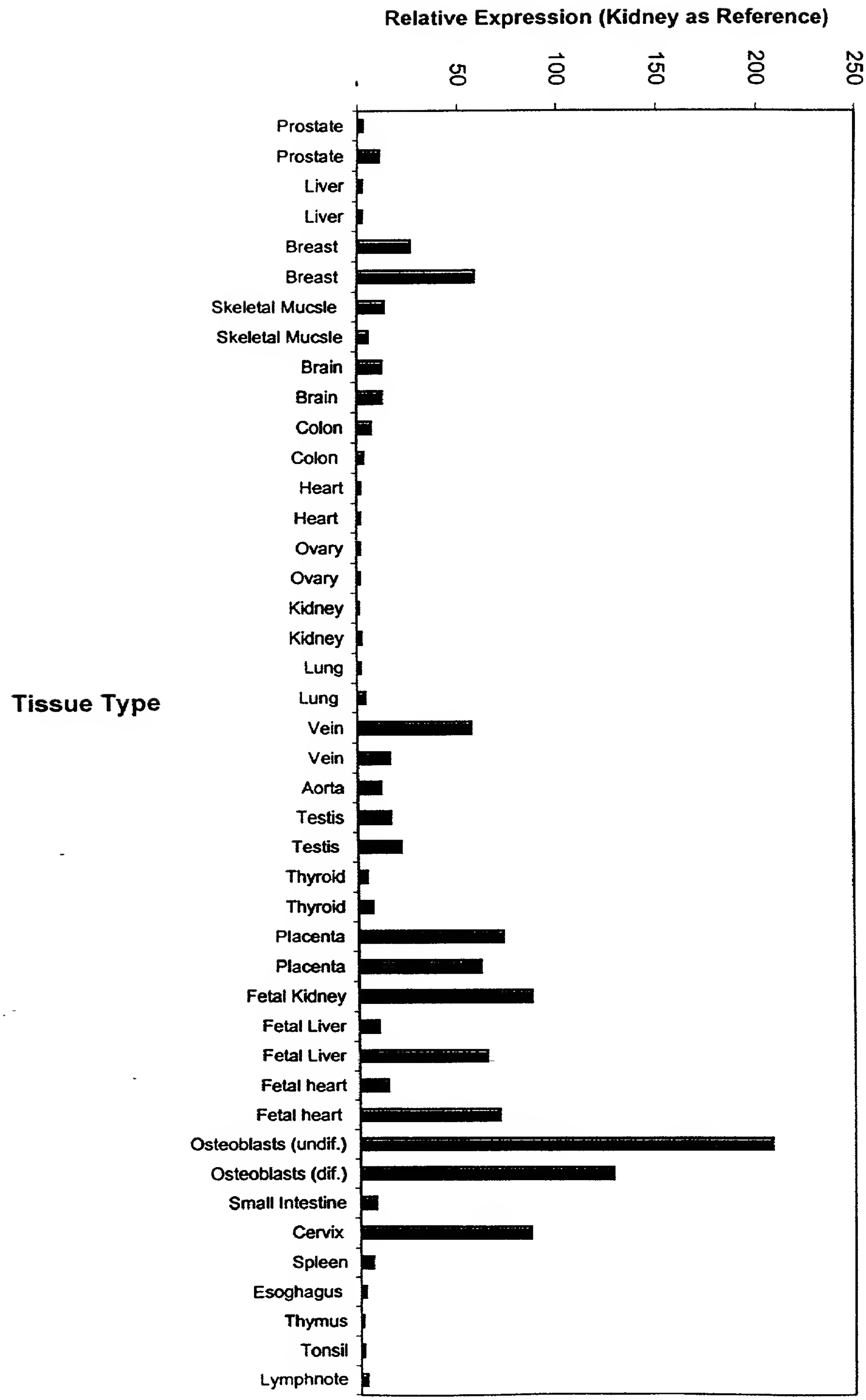
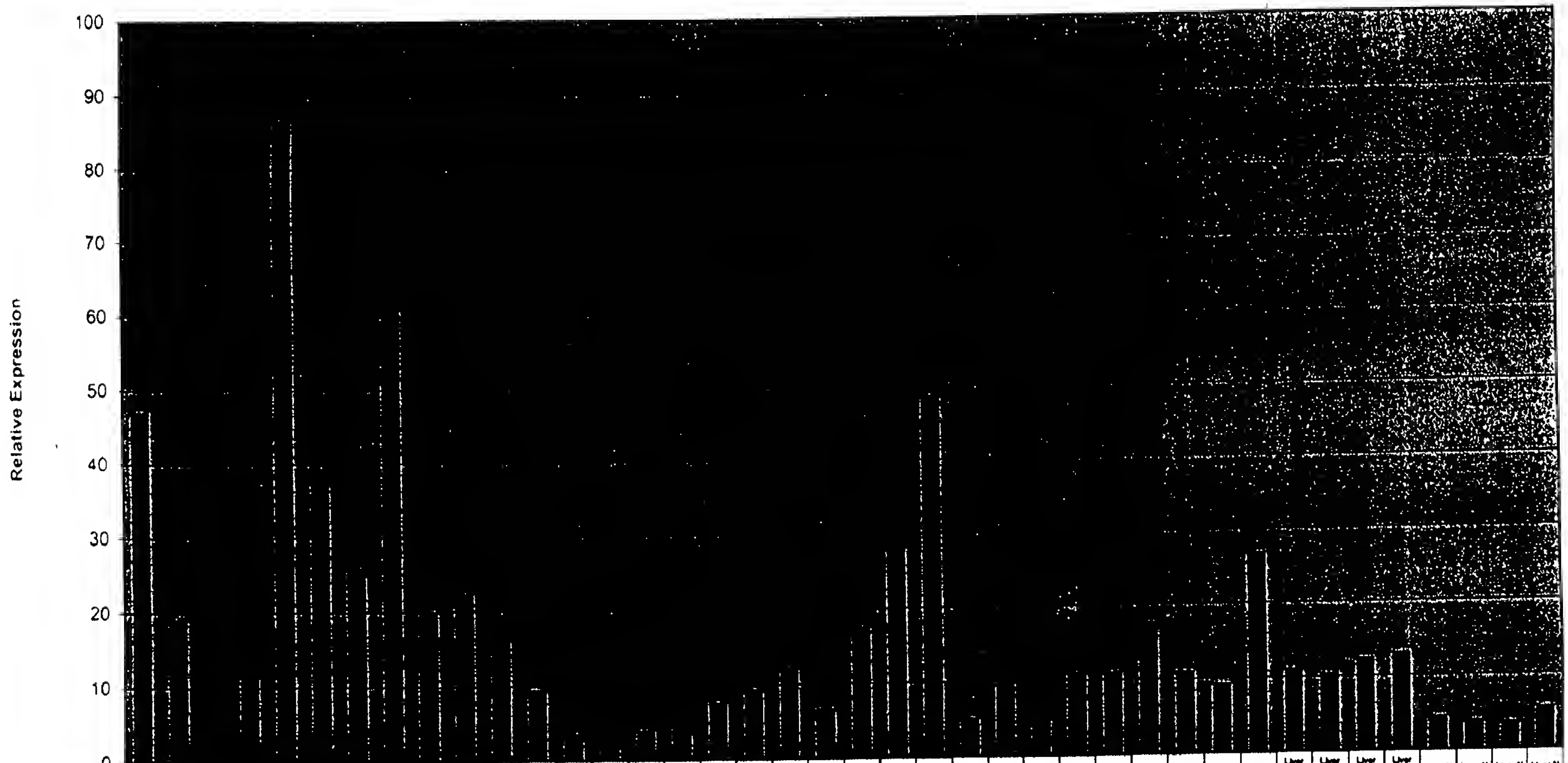

Relative Expression (Kidney as Reference)
50
100
150
200
250
Tissue Type
Prostate
Prostate
Liver
Liver
Breast
Breast
Skeletal Mucsle
Skeletal Mucsle
Brain
Brain
Colon
Colon
Heart
Heart
Ovary
Ovary
Kidney
Kidney
Lung
Lung
Vein
Vein
Aorta
Testis
Testis
Thyroid
Thyroid
Placenta
Placenta
Fetal Kidney
Fetal Liver
Fetal Liver
Fetal heart
Fetal heart
Osteoblasts (undif.)
Osteoblasts (dif.)
Small Intestine
Cervix
Spleen
Esoghagus
Thymus
Tonsil
Lymphnote

FIG. 10



	Breast N	Breast N	Breast N	Breast N	Breast T	Breast T	Breast T	Breast T	Breast T	Breast T	Breast T	Lung N	Lung N	Lung N	Lung T	Lung T	Lung T	Lung T	Lung T	Lung T	Lung T	Lung T	Colon N	Colon N	Colon N	Colon N	Colon T	Colon T	Colon T	Colon T	Colon T	Colon T	Liver Met	Liver Met	Liver Met	Liver Met	Liver N	Liver N	Liver N	Liver N
Relative Expression	46.86	18.96	1.00	17.38	86.82	37.27	25.72	60.76	19.84	22.34	16.26	4.94	3.34	9.90	4.94	4.94	7.39	9.13	12.06	9.90	17.27	28.15	48.50	4.94	10.09	4.94	10.78	10.89	17.38	10.82	9.08	28.63	10.93	10.30	12.25	12.91	4.30	3.88	3.48	8.41

Tissue Type

FIG. 11

FIG. 12A

```
GAATTCGGCACGAGGGCCGGCACCCCCGCGCCACCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGG  79

                             M   A   L   K   V   L   P   L   H   R   T   V   L   13
AAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG CTC 145

 F   A   A   I   L   F   L   L   H   L   A   C   K   V   S   C   E   T   G   D   33
TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA GAT 205

 C   R   Q   Q   E   F   K   D   R   S   G   N   C   V   L   C   K   Q   C   G   53
TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC GGA 265

 P   G   M   E   L   S   K   E   C   G   F   G   Y   G   E   D   A   Q   C   V   73
CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT GTG 325

 P   C   R   P   H   R   F   K   E   D   W   G   F   Q   K   C   K   P   C   A   93
CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT GCG 385

 D   C   A   L   V   N   R   F   Q   R   A   N   C   S   H   T   S   D   A   V  113
GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT GTC 445

 C   G   D   C   L   P   G   F   Y   R   K   T   K   L   V   G   F   Q   D   M  133
TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC ATG 505
```

FIG. 12B

E	C	V	P	C	G	D	P	P	P	P	Y	E	P	H	C	T	S	K	V	153
GAG	TGT	GTG	CCC	TGC	GGA	GAC	CCA	CCT	CCT	CCC	TAC	GAA	CCA	CAC	TGT	ACC	AGC	AAG	GTG	565
N	L	V	K	I	S	S	T	V	S	S	P	R	D	T	A	L	A	A	V	173
AAC	CTT	GTG	AAG	ATC	TCC	TCC	ACC	GTC	TCC	AGC	CCT	CGG	GAC	ACG	GCG	CTG	GCT	GCC	GTC	625
I	C	S	A	L	A	T	V	L	L	A	L	L	I	L	C	V	I	Y	C	193
ATC	TGC	AGT	GCT	CTG	GCC	ACG	GTG	CTG	CTC	GCC	CTG	CTC	ATC	CTG	TGT	GTC	ATC	TAC	TGC	685
K	R	Q	F	M	E	K	K	P	S	C	K	L	P	S	L	C	L	T	V	213
AAG	AGG	CAG	TTC	ATG	GAG	AAG	AAA	CCC	AGC	TGT	AAG	CTC	CCA	TCC	CTC	TGT	CTC	ACT	GTG	745
K	*																			215
AAG	TGA																			751

GCTTGTTAGCATTGTCACCCAAGAGTTCTCAAGACACCTGGCTGAGACCTAAGACCTTTAGAGCATCAACAGCTACTTA 830

GAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTCAGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCA 909

AGGCTACCAGGAAAAAATAAAAGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCGC 981

FIG. 13

```
GAATTCGGCACGAGGGCGTTTGGCGCGGAAGTGCTACCAAGCTGCGGAAAGCGTGAGTCTGGAGCACAGCACTGGCGAG  79

                              M   A   L   K   V   L   P   L   H   R   T   V      12
TAGCAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG  145

 L   F   A   A   I   L   F   L   L   H   L   A   C   K   V   S   C   E   T   G    32
CTC TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA  205

 D   C   R   Q   Q   E   F   K   D   R   S   G   N   C   V   L   C   K   Q   C    52
GAT TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC  265

 G   P   G   M   E   L   S   K   E   C   G   F   G   Y   G   E   D   A   Q   C    72
GGA CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT  325

 V   P   C   R   P   H   R   F   K   E   D   W   G   F   Q   K   C   K   P   C    92
GTG CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT  385

 A   D   C   A   L   V   N   R   F   Q   R   A   N   C   S   H   T   S   D   A   112
GCG GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT  445

 V   C   G   D   C   L   P   G   F   Y   R   K   T   K   L   V   G   F   Q   D   132
GTC TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC  505

 M   E   C   V   P   C   G   D   P   P   P   P   Y   E   P   H   C   E   *       151
ATG GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT GAG TGA      562

TGTGCCAAGTGGCAGCAGACCTTTAAAAAAAAAAGAAAAAAAAACAAACAAAAACAAAAAAAAAAAAAAAAAAAAAAAA  641

ATTTCCGCGGCCGC                                                                   655
```

FIG. 14A

```
      M A L K V L P L H R T V L F A A I L F L L H L A C K V S C E T G D C R Q Q E F K D R S G N C V L C K Majority
                        10                  20                  30                  40                  50
  1   M A L K V L P L H R T V L F A A I L F L L H L A C K V S C E T G D C R Q Q E F K D R S G N C V L C K muT127a
  1   M A L K V L P L H R T V L F A A I L F L L H L A C K V S C E T G D C R Q Q E F K D R S G N C V L C K muT127b
  1   M Y V W V Q Q - - - - - - - P T A L L L L A L T L G V T A R R L N C V K H T Y P S - G H K C - - C R ox40

      Q C G P G M E L S K E C G F G Y G E D A Q C V P C R P H R F K E D W G F Q K C K P C A D C A L V N R Majority
                        60                  70                  80                  90                 100
 51   Q C G P G M E L S K E C G F G Y G E D A Q C V P C R P H R F K E D W G F Q K C K P C A D C A L V N R muT127a
 51   Q C G P G M E L S K E C G F G Y G E D A Q C V P C R P H R F K E D W G F Q K C K P C A D C A L V N R muT127b
 41   E C Q P G H G M V S R C - - D H T R D T L C H P C E T G F Y N E A V N Y D T C K Q C T Q C N H R S G ox40

      F Q - R A N C S H T S D A V C G D C L P G F Y R K T K L V G F Q - D M E C V P C G D P P P P Y E P H Majority
                       110                 120                 130                 140                 150
101   F Q - R A N C S H T S D A V C G D C L P G F Y R K T K L V G F Q - D M E C V P C G D P P P P Y E P H muT127a
101   F Q - R A N C S H T S D A V C G D C L P G F Y R K T K L V G F Q - D M E C V P C G D P P P P Y E P H muT127b
 89   S E L K Q N C T P T Q D T V C - R C R P G T Q P R Q D - S G Y K L G V D C V P C - - P P G H F S P G ox40
```

FIG. 14B

```
    - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C E X X X X L X X X X X X X X X X X X X X  Majority
                    160                170                180                190                200
149 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C T S K V N L V K I - - - - - - - - - - -  muT127a
149 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C E .                                      muT127b
135 N N Q A C K P W T N C T L S G K Q T R H P A S D S L D A V C E D R S L L A T L L W E T Q R P T F R P  ox40

    X X X X X X X X X X X X X X X X X X X T X X X P X X X A X A X X X X X X L X X X X X L X X L L X L X  Majority
                    210                220                230                240                250
159 - - - - - - - - - - - - - - - - - S S T V S S P R D T A L A A V I C S A L A T V - - L L A L L I L C  muT127a
151                                                                                                      muT127b
185 T T V Q S T T V W P R T S E L P S P P T L V T P E G P A F A V L L G L G L G L L A P L T V L L A L Y  ox40

    X X X X X X X X X X X X X X C X X X S X X X X X X X X X X X X X X X X X K -                          Majority
                    260                270                280
190 V I Y C K R Q F M E K K P S C K L P S L C L T V - - - - - - - - - - - - K .                          muT127a
151                                                                                                      muT127b
235 L L R K A W R L P N T P K P C W G N S F R T P I Q E E H T D A H F T L A K I                          ox40
```

FIG. 15A

```
FASTA searches a protein or DNA sequence data bank
 version 2.0u53 July, 1996
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

 inputs/nb589712.tmp :  215 aa
 > T127Atm473200aa: 215 aa
 vs  library
 searching inputs/nb782215.tmp library

    423 residues in     1 sequences
The best scores are:                                    initn init1 opt
 Patent Protein W70387 - (untitled)                       982 982   982

>> Patent Protein W70387 - (untitled)                   (423 aa)
initn:  982  init1:  982  opt:  982
Smith-Waterman score: 982;    85.7% identity in 203 aa overlap

               10        20        30        40        50        60

 T127A MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK

       X:::::  .  ..:. ...:  :.:::.::::::::::::.::::::: :.:::::::::::

       MALKVLLEQEKTFFTLLVLLGYLSCKVTCETGDCRQQEFRDRSGNCVPCNQCGPGMELSK

               10        20        30        40        50        60
```

FIG. 15B

```
              70        80        90       100       110       120
T127A ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG
      ::::::::::::: :: ::::::::::::::: :::.:::::.:::: ::::.:::::::
      ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG
              70        80        90       100       110       120

             130       140       150       160       170       180
T127A FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT
      :::::::::::::::::::::::::::::.::::::::.::.::::::::::::::::::
      FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
             130       140       150       160       170       180

             190       200       210
T127A VLLALLILCVIYCKRQFMEKKPSCKLPSLCLTVKN
      :::::::::::::::::::::::X
      VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCLDPRQLHEYAHRACCQCRRD
             190       200       210       220       230       240
```

FIG. 16A

```
 FASTA searches a protein or DNA sequence data bank
 version 2.0u53 July, 1996
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

 inputs/nb504897.tmp :  981 aa
 > Atm472300: 981 aa
 vs  library
 searching inputs/nb658900.tmp library

   1496 residues in     1 sequences
The best scores are:                                initn init1 opt
 Patent Nucleotide V33362 - (untitled)               2575 2575 2861

>> Patent Nucleotide V33362 - (untitled)                 (1496 aa)
initn: 2575  init1: 2575  opt: 2861
Smith-Waterman score: 2888;    70.6% identity in 922 aa overlap

                 40        50        60        70        80        90
Atm47 CCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGGAAGGAATAAACACG
                                                   X:..:. .. :      :. :::::: ::.
                                                   GGGAACGTAGAACTCTCCAACAATAAATACA
                                                           10        20        30
```

FIG. 16B

```
             100       110       120       130       140       150
Atm47  TTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGCTCTTCGCTGC
       ::::.:.:::.  :::::. : ::.:: :::: .  .::: ..:: .. : : :::.::
       TTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTTTTTCACTCT
               40        50        60        70        80        90

             160       170       180       190       200       210
Atm47  CATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGCAGGCA
        .:. : :: :::  : :  :: :::::::::::: ::: ::::: ::::: :: ::.::
       TTTAGTATTACTAGGCTATTTGTCATGTAAAGTGACTTGTGAAACAGGAGACTGTAGACA
               100       110       120       130       140       150
```

FIG. 16C

```
          220       230       240       250       260       270
Atm47 GCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCGGACCTGGCAT
      :::.:::::::.::::::.::::::::::::: : :::::: ::::: ::.::.:::::
      GCAAGAATTCAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCAT
            160       170       180       190       200       210

          280       290       300       310       320       330
Atm47 GGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTGCAG
      ::::::::: ::::::::::::::::::::::::::::::::::::::::: : ::: :
      GGAGTTGTCTAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCG
            220       230       240       250       260       270
```

FIG. 16D

```
               340       350       360       370       380       390
Atm47 GCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTGCGGACTGTGC
      :: :::: ::::::::::.:::::::: ::::::::.:: ::::: :::  :::::: ::
      GCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGC
                 280       290       300       310       320       330

               400       410       420       430       440       450
Atm47 GCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTGTCTGCGGGGA
      . ::::::::::::::::::.::: :: :: :::  :::::::::::: .::::::::::
      AGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAGCCACCAGTGATGCCATCTGCGGGGA
                 340       350       360       370       380       390
```

FIG. 16E

```
            460       470       480       490       500       510
Atm47 CTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGT
      :::: :::::::::::::  ::::::: ::::: :: :: ::::::::::::::::::::
      CTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGT
              400       410       420       430       440       450

            520       530       540       550       560       570
Atm47 GCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGGTGAACCTTGT
      ::: :: ::::::::.:::::::: ::::::::.::::::.:::::::::: ::::: ::
      GCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGT
              460       470       480       490       500       510
```

FIG. 16F

```
          580       590       600       610       620       630
Atm47 GAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCGTCATCTGCAG
      ::::::: : ::::: : :::::::::.::::::::::::::::::::::: ::::::::
      GAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAG
            520       530       540       550       560       570

          640       650       660       670       680       690
Atm47 TGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACTGCAAGAGGCA
       ::::::::::: :: ::::: :::::::::::::: ::::::::::: :: :::::.::
      CGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCATCTATTGTAAGAGACA
            580       590       600       610       620       630
```

FIG. 16G

```
         700       710       720       730       740       750
Atm47 GTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCCTCTGTCTCACTGTGAAGTGAGC
      ::: :::::::::::::::::::: .  :: : .:: :.  :.:. .:.::. :. : ::
      GTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACA-GGACATTCAGTACAACG-GC
             640       650       660       670       680

         760       770       780       790       800       810
Atm47 TTGTTAGCATT-GTCACCCAAGAGTTCTCAAGACACCT-GGCTGAGACCTAAGA-CCTTT
      :  : :::. : :: .:  .: ::. :^:v.  :.::. :. :..: ::. ::: :::
      TC-TGAGCTGTCGTGTCTTGACAGACCTCAG--CTCCACGAATATGCCCACAGAGCCT--
   690       700       710          720       730       740
```

FIG. 16H

```
             820       830       840       850       860       870
Atm47 AGAGCATCAACAGCTACTTAGAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTC
         ::. : : .:: .:  .::   :. ..:::::.  ..::.:::  : : : .. :::
      ---GCTGCCAGTGCCGCCGTGA---CTCAGTGCAGACCTGCGGGCCGGTGC-GCTTGCTC
            750       760          770       780         790

             880       890       900       910       920       930
Atm47 AGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCAAGGCTACCAGGAAAAAATAAA
          : :::..: : :: ::. .::::  :: .: : :::  :  ::.: .: . .:...
      C---CATCCATGTGCTG-TGAGGAGGCC-TGCAGCCCCAA--C--CCGGCGACTCTTGGT
         800       810        820        830           840
```

FIG. 16I

```
           940       950       960       970         980
Atm47 AGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGC--GGCCGC
      .:: :  :. :  ::. :.  :.. .. :.. ::.::: .:: ::  .::::
      TGTGGGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCAGCCGGGGAGATG
     850       860       870       880       890       900

      GTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGG
     910       920       930       940       950       960
```

GAATTCGGAACGAGGGGAACCTAATTCTCCTGAGGCTGAGGGAGGGTGGAGGGTCTCAAGGCAACGCTGGCCCCACGAC 79

GGAGTGCCAGGAGCACTAACAGTACCCTTAGCTTGCTTTCCTCCTCCCTCCTTTTTATTTTCAAGTTCCTTTTTATTTC 158

TCCTTGCGTAACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCCGCCACCTCCTTGCTACCCCACT 237

M P A S S P F L L A P 11

CTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC ATG CCA GCC TCA TCT CCT TTC TTG CTA GCC CCC 305

K G P P G N M G G P V R E P A L S V A L 31

AAA GGG CCT CCA GGC AAC ATG GGG GGC CCA GTC AGA GAG CCG GCA CTC TCA GTT GCC CTC 365

W L S W G A A L G A V A C A M A L L T Q 51

TGG TTG AGT TGG GGG GCA GCT CTG GGG GCC GTG GCT TGT GCC ATG GCT CTG CTG ACC CAA 425

Q T E L Q S L R R E V S R L Q G T G G P 71

CAA ACA GAG CTG CAG AGC CTC AGG AGA GAG GTG AGC CGG CTG CAG GGG ACA GGA GGC CCC 485

S Q N G E G Y P W Q S L P E Q S S D A L 91

TCC CAG AAT GGG GAA GGG TAT CCC TGG CAG AGT CTC CCG GAG CAG AGT TCC GAT GCC CTG 545

E A W E N G E R S R K R R A V L T Q K Q 111

GAA GCC TGG GAG AAT GGG GAG AGA TCC CGG AAA AGG AGA GCA GTG CTC ACC CAA AAA CAG 605

K K Q H S V L H L V P I N A T S K D D S 131

AAG AAG CAG CAC TCT GTC CTG CAC CTG GTT CCC ATT AAC GCC ACC TCC AAG GAT GAC TCC 665

D V T E V M W Q P A L R R G R G L Q A Q 151

GAT GTG ACA GAG GTG ATG TGG CAA CCA GCT CTT AGG CGT GGG AGA GGC CTA CAG GCC CAA 725

G Y G V R I Q D A G V Y L L Y S Q V L F 171

GGA TAT GGT GTC CGA ATC CAG GAT GCT GGA GTT TAT CTG CTG TAT AGC CAG GTC CTG TTT 785

Q D V T F T M G Q V V S R E G Q G R Q E 191

CAA GAC GTG ACT TTC ACC ATG GGT CAG GTG GTG TCT CGA GAA GGC CAA GGA AGG CAG GAG 845

T L F R C I R S M P S H P D R A Y N S C 211

ACT CTA TTC CGA TGT ATA AGA AGT ATG CCC TCC CAC CCG GAC CGG GCC TAC AAC AGC TGC 905

Y S A G V F H L H Q G D I L S V I I P R 231

TAT AGC GCA GGT GTC TTC CAT TTA CAC CAA GGG GAT ATT CTG AGT GTC ATA ATT CCC CGG 965

A R A K L N L S P H G T F L G F V K L * 251

GCA AGG GCG AAA CTT AAC CTC TCT CCA CAT GGA ACC TTC CTG GGG TTT GTG AAA CTG TGA 1025

TTGTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAAGAGCTGAGTATATAA 1104

AGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTCCCCGTTCCTCACTTTTCCCTTTTCATTCCCAC 1183

CCCCTAGACTTTGATTTTACGGATATCTTGCTTCTGTTCCCCATGGAGCTCCGAATTCTTGCGTGTGTGTAGATGAGGG 1262

GCGGGGGACGGGCGCCAGGCATTGTTCAGACCTGGTCGGGGCCCACTGGAAGCATCCAGAACAGCACCACCATCTAGCG 1341

GCCGC 1346

Fig. 17

```
T118 pileup.msf  MSF: 286
1913 ..
Name: TRASH  Len: 286  Check:  7625    Weight: 1.00
Name: TNF    Len: 286  Check:  5421    Weight: 1.00
Name: tweak  Len: 286  Check:  8867    Weight: 1.00
//
       1                                                          60
TRASH  MPASSPFL...LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQS
  TNF  MSTESMIRDVELAEEALPKKTGGP...QGSRRCLFLSLFSFL........IVAGATTLFC
tweak  MAARR........SQRRRGRRGEPGTALLVPLALGLGL.....ALAC.LGLLLAVVSLGS

       61                                                        120
TRASH  LRREVSRLQ.GTGGPSQNGEGYPWQ.SLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH
  TNF  L......LHFGVIGPQR..EEFPRDLSLISPLAQAV.......RSSSRTP.......SDK
tweak  .RASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARR

       121                                                       180
TRASH  SV.....LHLVPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR.....IQDAGVYLL
  TNF  PV.....AHVVANPQAE......GQLQWLN..RRANALLANGVELRDNQLVVPSEGLYLI
tweak  AIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA..RINSSSPLRYNRQIGEFIVTRAGLYYL

       181                                                       240
TRASH  YSQVLFQDVTFTMGQVVSREGQGRQETLFR..............CIRSMPSHPDRA....
  TNF  YSQVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLL..SAIKSPCQRETPEGAEAK..PW
tweak  YCQVHFDEG................KAVYL.KLDLLVDGVLALRCLEEFSATAASSLGPQ

       241                                            286
TRASH  YNSCYSAGVFHLHQGDILSV.IIPRARAKLNLSPHG.TFLGFVKL.
  TNF  YEPIYLGGVFQLEKGDRLSA.EINRPDY.LDFAESGQVYFGIIAL.
tweak  LRLCQVSGLLALRPGSSLRIRTLPWAHLK...AAPFLTYFGLFQVH
```

Fig. 18

Nucleotide and Amino Acid Sequence of Human βDSF

```
GTCGACCCAC GCGTCCGGCA GGATGTTTGC AGTGTCGCGC CCAGGGCTCT GAGACTGAGC    60

CTGCCATCCA CTCGCACGCC TTTCTTTCAG GGCTTTTCGG CTGTTGGCTA CACTGATGTG   120

ACCCCCCTCC CTTTTTGGA ATG ATG GGG ATC TTT TTG GTG TAT GTT GGA TTT    172
                     Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe
                      1               5                   10

GTT TTC TTT TCC GTT TTA TAT GTA CAA CAA GGG CTT TCT TCT CAA GCA     220
Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
            15                  20                  25

AAA TTT ACC GAG TTT CCG CGG AAC GTG ACG GCG ACC GAG GGG CAG AAT     268
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn
        30                  35                  40

GTG GAG ATG TCC TGC GCC TTC CAG AGC GGC TCC GCC TCG GTG TAT CTG     316
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu
    45                  50                  55

GAG ATC CAA TGG TGG TTC CTG CGG GGG CCG GAG GAC CTG GAT CCC GGG     364
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly
60                  65                  70                  75

GCC GAG GGG GCC GGC GCG CAG GTG GAG CTC TTG CCC GAC AGA GAC CCG     412
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro
                80                  85                  90

GAC AGC GAC GGG ACC AAG ATC AGC ACA GTG AAA GTC CAA GGC AAT GAC     460
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp
            95                  100                 105

ATC TCC CAC AAG CTT CAG ATT TCC AAA GTG AGG AAA AAG GAT GAA GGC     508
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly
        110                 115                 120

TTA TAT GAG TGC AGG GTG ACT GAT GCC AAC TAC GGG GAG CTT CAG GAA     556
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu
    125                 130                 135

CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT GCC CGC     604
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg
140                 145                 150                 155

AGA ATG CAG GCC TTC GAA GCC TCG CCC ATG TGG CTG CAG GAT ATG AAG     652
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys
                160                 165                 170

CCC CGC AAG AAC GTC TCC GCA GCC ATC CCC AGC AGC ATC CAT GGC TCT     700
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser
            175                 180                 185

GCC AAC CAA CGA ACG CAC TCC ACC TCC AGC CCT CAA GTG GTA GCC AAA     748
Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys
        190                 195                 200

ATC CCC AAA CAA AGT CCA CAA TCA GGT ATG GAA ACC CAT TTC GAG CCT     796
```

Fig. 19A

```
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro
    205                 210                 215

TTT ATT TTA CCA CTC ACA AAC GCT CCA CAG AAA GGT CAG TCG TAT AGA      844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg
220                 225                 230                 235

GTA GAC AGA TTT ATG AAT GGT GAT TTT TAAAATCGGA GACCTAGTTC            891
Val Asp Arg Phe Met Asn Gly Asp Phe
                240

AGTGCAAGTG ATTATGAGAG GTGAGCACTG AGCCTGCACC AATTCACTCA GAGCTCAAAG    951

CATGTGGGTG CACCCCGTCA GTCCCCTAGT GGTGCTTCAT TTCCAGGGCA TCTGAGAGCT   1011

GGACTCTGGT TTTTATCCTT TCTGTATTTA CACATTATAA GAACAATAAA TCATGTAATG   1071

TTGGTTACAT TACAAAAAAA AAAAAAAAAA AAAAAAAAGG GCGGCCGC                1119
```

Fig. 19B

Nucleotide and Amino Acid Sequence of Murine BDSF

CACGCGTCCG CAGCCAGCCG GCGGCGGAGA CACTTCACGG CGTGGCAACC CGGGTCTGTG 60

CCTTGAAGCC TCCGGATCGC AGCCAGCTCG GTCCATCCCT CACTAGTCGC AATCCCCTGT 120

GTCCAAGCTA CTCTTTGCTA TGAGCGGCAG CATGCGTGCA GTATCGCGCC CCAGGCTCTG 180

AGAGCAGCCT GCGGACACGC TTGCCTATCT GTCTTTTTAG GTTTTGGGGC TCTGGGCTAC 240

ACGGATGTGC CCCACTCCCT TGGCATG ATG GGG ATC TTT TTG GCG TCT GTT 291
Met Gly Ile Phe Leu Ala Ser Val
1 5

GGA TTT ATG TTC TTT TCC GTG TTA TAT GTA CAA CAA GGG CTT TCT TCT 339
Gly Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser
10 15 20

CAA GCA AAA TTT ACC GAG TTG CCG AGA AAT GTG ACT GCT ACC GAA GGG 387
Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly
25 30 35 40

CAA AAT GTG GAG ATG TCC TGT GCT TTC CAA AGC GGC TCT GCT TCA GTG 435
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
45 50 55

TAC CTG GAG ATC CAG TGG TGG TTC CTT CGG GGG CCA GAG GAC CTG GAG 483
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu
60 65 70

CAA GGC ACG GAG GCT GCA GGC TCG CAG GTG GAG CTC TTA CCC GAC AGA 531
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
75 80 85

GAC CCG GAC AAC GAT GGG ACC AAG ATT AGT ACA GTG AAA GTC CAA GGC 579
Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
90 95 100

AAT GAT ATC TCC CAC AAG CTT CAG ATA TCC AAA GTG AGA AAA AAG GAT 627
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
105 110 115 120

GAA GGT TTA TAC GAG TGC AGG GTG ACT GAC GCT AAC TAC GGG GAG CTT 675
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
125 130 135

CAG GAA CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT 723
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
140 145 150

GCT CGG AGG ATG CAG GCC TTT GAA GCC TCA CCT ATG TGG CTG CAA GAC 771
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
155 160 165

ACG AAG CCT CGA AAG AAC GCA TCA TCG GTG GTT CCC AGC AGC GTC CAC 819
Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His
170 175 180

AAC TCT GCC AAC CAA CGA ATG CAC TCC ACC TCC AGC CCT CAA GCG GTA 867

Fig. 20A

Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val
185 190 195 200

GCC AAA ATC CCC AAG CAA AGT CCA CAA TCA GCA AAG AGC AAA TCG CCT 915
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro
205 210 215

GTA AAA TCT ACG GAG CGG ACA GCA AAG TTG ACC CTA TAC TCC AAG CAC 963
Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His
220 225 230

CAT TCT GCA CCC CTG TAC TCT AGT TAT CTA CAC AAG GAG CAT CAG CTT 1011
His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu
235 240 245

CCG GAA GCA TAAGTGAAGA CACTGTCACA CGCTTTATTG ATAATATTTT 1060
Pro Glu Ala
250

CTTTGGGAAG TTGCTGATCT TTTATTTCAA GAGAATTAAT GGGAAGAGAT AGGACATTTT 1120

CCAATTACAA GACCAATTTT TTTCCTTTTA TTTCAACAAA TAAAACCTGC ATTTCACTGA 1180

CTGCTCAGGA GTTGGCCTGA ATGACATCAG TATACTAAAT ATTTCCATGG ATTCCACCAA 1240

TTTCCTAACG AGGGACACCT AATCTTCAAG AAGCAAACAA AGATGGAAAA CCTAAGAACC 1300

ACAAACTGTC TCATACAGCA CCCCAGCTGA GGAACAAAAC AAATAGCTAA ATGCTGACCA 1360

TGGCAAATCA ACATCAGACA ACTTTATTTT ACATATGGAA TAATCAAAGA AAGTTTTTTT 1420

TTTACTTCCT TTTTGCCCCC TGGAATTTAT CTTGGAGTTT CCCTTTTTTC CTTGATTGCC 1480

GTTTTCGTTC AATGGTAGCA AGTGCCAATT ATGGCCAATC CTTGTCAATC CTGGAAGGTT 1540

TATATTCATA TACATTGAGT GTGGTATATA TCAATGTATT TTAATTCATT TGGCAATTTC 1600

TGTATAGGCA AACCTGGCAA ATTCTGTAAA TTGCTTATAG TATGTGTGAT ATGACTTCAA 1660

GGTAGATAGG CTATGATGCT CATGCAAGCT GACTTTCTTC ATTCTATATA CAAATATATT 1720

CATGAGCATA TATTAGGCCA CCAACTTCTT TTCCTAAAGA ATTATTTTTC ATTTGTACCT 1780

CATGTATTTT GTGAATTTTG TAGTATATTT CTCTGTTCCA CTAGTTTGAC CGCTACAGTT 1840

TGTCTCTGTT GTCCTCTACT TCCTTCTGGA AAAATTTAAA ATTGTGTATG TCTCTGATAA 1900

ATGAATTAAT TTTGTTGTGT GTATGCTATG TTGGAATTTG CTGTGTTCTT TTAAACATGT 1960

ATTTATTAAG GTTTGGGGAT CTTGAGTTGA GTCTGAAGAA TGCACACCTG GTTTTTGACA 2020

GAGTTCCTCA TGTTACCAAT ATTCTATCTC AGAGAAAGAA AGACACCAAG TGGGAAAACT 2080

AAGAAGACAT TTTGACTTCC CAAGATCCTG GAAGAGCACT TCACACTCTG ACTAAATAAT 2140

GTTGCTTTTT TTGTTCTTCA AGACTTTTTT GTAGCTTTGT CTTTCTGTTA GTTGCTGCTA 2200

ATTATATTTT AATGTCTACT AATTAAAAAT TAAAATGTGA TTGTTGGCTG AATACAATAT 2260

Fig. 20B

GCAAATGACT GCAAAGCCCA TACTGAAGAA AATAGATGTT TAATCTTCAC TCAATAATTA 2320

TAATTTTAAA TAGTTCATCA TTATTTTTTG ACCTTATGAT ATTTTGTTTA GACCTGTTCT 2380

AATTACATCT TTCTCTGGCA AAGAAAGATA GAACAATCAA TACATTCCCT CTTACAGTAT 2440

GGAATGGTTG TGGCTTAAGA AAGAATGCAT CCAGATGGTC TTCCAGAGAG ATTATTTTAT 2500

TTTCATTATA AAACCAGAAA CCATATATGT AGGAATGGTT CATTCCTAAT GTAAGGCCAT 2560

AAATTGTAGC TTGAAGGCAA GGAATACATT TGTTTTTTTA TGGTAAAGGA CTGGCCTCTG 2620

ACATGCACTT ATAAGCAATG TGAATATTTT CATAATATGC TTGACATTCT CCTTTAACAA 2680

ATATTGTTTT ATGGTAAATC TTTCCTTGCC ATTTTTCTTC TTTCATTTGA TTCATTATTT 2740

CATTCTAATG AAGAAAATAA AGGTTTAATT ATGATACTTT ATTAACATAC AAATGTATTT 2800

TCTTTCTAAG TTAAATATCT GAAAGTTGTA TAAAATGATG GTAGAGAAAT ATTACTCATT 2860

CGGTTTCTTT GAGCTTTAAG AATCCCATAC ATTGCAGTAT ATATTAGAAT ACTGATTTAA 2920

CATCAAACTG GGGGGGAAAA TCATGTATTA TACTTTTACT CAATGTCTAG GTAATGGATT 2980

CAGCTAATTT TACAGCAAGC CAAATGTGTA CCCGTATCAG TAATGTTCAC CATGCTTGTA 3040

ATAAAAGGGC ATATGCTAGT TTTGGAAGAA TGCTCATTAG ATTCATTGTA TCAGTGTCCA 3100

AAATAATAAA GACCTGTTTA TCACTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3160

AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCCGC 3196

Fig. 20C

Alignment of Human BDSF (hT122) and Murine BDSF (mT122)

```
>_ hT122                                              244 aa vs.
>_ mT122                                              251 aa
scoring matrix: , gap penalties: -12/-2
77.4% identity;        Global alignment score: 1236

                 10        20        30        40        50        60
hT122    MMGIFLVYVGFVFFSVLYVQQGLSSQAKFTEFPRNVTATEGQNVEMSCAFQSGSASVYLE
         : ::::. :::.::::::::::::::::::::.:::::::::::::::::::::::::::
mT122    M-GIFLASVGFMFFSVLYVQQGLSSQAKFTELPRNVTATEGQNVEMSCAFQSGSASVYLE
                 10        20        30        40         50

                 70        80        90       100       110       120
hT122    IQWWFLRGPEDLDPGAEGAGAQVELLPDRDPDSDGTKISTVKVQGNDISHKLQISKVRKK
         ::::::::::::.  :.:.::.::::::::::::.:::::::::::::::::::::::::
mT122    IQWWFLRGPEDLEQGTEAAGSQVELLPDRDPDNDGTKISTVKVQGNDISHKLQISKVRKK
        60        70        80        90       100       110

                130       140       150       160       170       180
hT122    DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDMKPRKNVSAAI
         ::::::::::::::::::::::::::::::::::::::::::::::::: :::::.:...
mT122    DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDTKPRKNASSVV
      120       130       140       150       160       170

                190       200       210            220       230
hT122    PSSIHGSANQRTHSTSSPQVVAKIPKQSPQSG-----METHFEPFILPLTNAPQKG---Q
         :::.:.::::: ::::::::.:::::::::::.        ...  .   : :  .  ...   .
mT122    PSSVHNSANQRMHSTSSPQAVAKIPKQSPQSAKSKSPVKSTERTAKLTLYSKHHSAPLYS
      180       190       200       210       220       230

                240
hT122    SYRVDRFMNGDF
         ::   . . .
mT122    SYLHKEHQLPEA
      240       250

 Elapsed time:  0:00:00
```

Fig. 21

```
GTCGACCCACGCGTCCGGAGCCCGGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGG  79

GCCCGACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCGCCTCCCGGGACAGAA  158

  M   C   S   R   V   P   L   L   L   P   L   L   L   L   A   L   G   P      19
G ATG TGC TCC AGG GTC CCT CTG CTG CTG CCG CTG CTC CTG CTA CTG GCC CTG GGG CCT     216

 G   V   Q   G   C   P   S   G   C   Q   C   S   Q   P   Q   T   V   F   C   T    39
GGG GTG CAG GGC TGC CCA TCC GGC TGC CAG TGC AGC CAG CCA CAG ACA GTC TTC TGC ACT   276

 A   R   Q   G   T   T   V   P   R   D   V   P   P   D   T   V   G   L   Y   V    59
GCC CGC CAG GGG ACC ACG GTG CCC CGA GAC GTG CCA CCC GAC ACG GTG GGG CTG TAC GTC   336

 F   E   N   G   I   T   M   L   D   A   G   S   F   A   G   L   P   G   L   Q    79
TTT GAG AAC GGC ATC ACC ATG CTC GAC GCA GGC AGC TTT GCC GGC CTG CCG GGC CTG CAG   396

 L   L   D   L   S   Q   N   Q   I   A   S   L   P   S   G   V   F   Q   P   L    99
CTC CTG GAC CTG TCA CAG AAC CAG ATC GCC AGC CTG CCC AGC GGG GTC TTC CAG CCA CTC   456

 A   N   L   S   N   L   D   L   T   A   N   R   L   H   E   I   T   N   E   T    119
GCC AAC CTC AGC AAC CTG GAC CTG ACG GCC AAC AGG CTG CAT GAA ATC ACC AAT GAG ACC   516

 F   R   G   L   R   R   L   E   R   L   Y   L   G   K   N   R   I   R   H   I    139
TTC CGT GGC CTG CGG CGC CTC GAG CGC CTC TAC CTG GGC AAG AAC CGC ATC CGC CAC ATC   576
```

FIG. 22A

```
 Q   P   G   A   F   D   T   L   D   R   L   L   E   L   K   L   Q   D   N   E    159
CAG CCT GGT GCC TTC GAC ACG CTC GAC CGC CTC CTG GAG CTC AAG CTG CAG GAC AAC GAG   636

 L   R   A   L   P   P   L   R   L   P   R   L   L   L   L   D   L   S   H   N    179
CTG CGG GCA CTG CCC CCG CTG CGC CTG CCC CGC CTG CTG CTG CTG GAC CTC AGC CAC AAC   696

 S   L   L   A   L   E   P   G   I   L   D   T   A   N   V   E   A   L   R   L    199
AGC CTC CTG GCC CTG GAG CCC GGC ATC CTG GAC ACT GCC AAC GTG GAG GCG CTG CGG CTG   756

 A   G   L   G   L   Q   Q   L   D   E   G   L   F   S   R   L   R   N   L   H    219
GCT GGT CTG GGG CTG CAG CAG CTG GAC GAG GGG CTC TTC AGC CGC TTG CGC AAC CTC CAC   816

 D   L   D   V   S   D   N   Q   L   E   R   V   P   P   V   I   R   G   L   R    239
GAC CTG GAT GTG TCC GAC AAC CAG CTG GAG CGA GTG CCA CCT GTG ATC CGA GGC CTC CGG   876

 G   L   T   R   L   R   L   A   G   N   T   R   I   A   Q   L   R   P   E   D    259
GGC CTG ACG CGC CTG CGG CTG GCC GGC AAC ACC CGC ATT GCC CAG CTG CGG CCC GAG GAC   936

 L   A   G   L   A   A   L   Q   E   L   D   V   S   N   L   S   L   Q   A   L    279
CTG GCC GGC CTG GCT GCC CTG CAG GAG CTG GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG   996

 P   G   D   L   S   G   L   F   P   R   L   R   L   L   A   A   A   R   N   P    299
CCT GGC GAC CTC TCG GGC CTC TTC CCC CGC CTG CGG CTG CTG GCA GCT GCC CGC AAC CCC  1056

 F   N   C   V   C   P   L   S   W   F   G   P   W   V   R   E   S   H   V   T    319
TTC AAC TGC GTG TGC CCC CTG AGC TGG TTT GGC CCC TGG GTG CGC GAG AGC CAC GTC ACA  1116
```

FIG. 22B

```
L   A   S   P   E   E   T   R   C   H   F   P   P   K   N   A   G   R   L   L     339
CTG GCC AGC CCT GAG GAG ACG CGC TGC CAC TTC CCG CCC AAG AAC GCT GGC CGG CTG CTC  1176

L   E   L   D   Y   A   D   F   G   C   P   A   T   T   T   T   A   T   V   P     359
CTG GAG CTT GAC TAC GCC GAC TTT GGC TGC CCA GCC ACC ACC ACC ACA GCC ACA GTG CCC  1236

T   T   R   P   V   V   R   E   P   T   A   L   S   S   S   L   A   P   T   W     379
ACC ACG AGG CCC GTG GTG CGG GAG CCC ACA GCC TTG TCT TCT AGC TTG GCT CCT ACC TGG  1296

L   S   P   T   A   P   A   T   E   A   P   S   P   P   S   T   A   P   P   T     399
CTT AGC CCC ACA GCG CCG GCC ACT GAG GCC CCC AGC CCG CCC TCC ACT GCC CCA CCG ACT  1356

V   G   P   V   P   Q   P   Q   D   C   P   P   S   T   C   L   N   G   G   T     419
GTA GGG CCT GTC CCC CAG CCC CAG GAC TGC CCA CCG TCC ACC TGC CTC AAT GGG GGC ACA  1416

C   H   L   G   T   R   H   H   L   A   C   L   C   P   E   G   F   T   G   L     439
TGC CAC CTG GGG ACA CGG CAC CAC CTG GCG TGC TTG TGC CCC GAA GGC TTC ACG GGC CTG  1476

Y   C   E   S   Q   M   G   Q   G   T   R   P   S   P   T   P   V   T   P   R     459
TAC TGT GAG AGC CAG ATG GGG CAG GGG ACA CGG CCC AGC CCT ACA CCA GTC ACG CCG AGG  1536

P   P   R   S   L   T   L   G   I   E   P   V   S   P   T   S   L   R   V   G     479
CCA CCA CGG TCC CTG ACC CTG GGC ATC GAG CCG GTG AGC CCC ACC TCC CTG CGC GTG GGG  1596

L   Q   R   Y   L   Q   G   S   S   V   Q   L   R   S   L   R   L   T   Y   R     499
CTG CAG CGC TAC CTC CAG GGG AGC TCC GTG CAG CTC AGG AGC CTC CGT CTC ACC TAT CGC  1656
```

FIG. 22C

```
N   L   S   G   P   D   K   R   L   V   T   L   R   L   P   A   S   L   A   E     519
AAC CTA TCG GGC CCT GAT AAG CGG CTG GTG ACG CTG CGA CTG CCT GCC TCG CTC GCT GAG  1716

Y   T   V   T   Q   L   R   P   N   A   T   Y   S   V   C   V   M   P   L   G     539
TAC ACG GTC ACC CAG CTG CGG CCC AAC GCC ACT TAC TCC GTC TGT GTC ATG CCT TTG GGG  1776

P   G   R   V   P   E   G   E   E   A   C   G   E   A   H   T   P   P   A   V     559
CCC GGG CGG GTG CCG GAG GGC GAG GAG GCC TGC GGG GAG GCC CAT ACA CCC CCA GCC GTC  1836

H   S   N   H   A   P   V   T   Q   A   R   E   G   N   L   P   L   L   I   A     579
CAC TCC AAC CAC GCC CCA GTC ACC CAG GCC CGC GAG GGC AAC CTG CCG CTC CTC ATT GCG  1896

P   A   L   A   A   V   L   L   A   A   L   A   A   V   G   A   A   Y   C   V     599
CCC GCC CTG GCC GCG GTG CTC CTG GCC GCG CTG GCT GCG GTG GGG GCA GCC TAC TGT GTG  1956

R   R   G   R   A   M   A   A   A   A   Q   D   K   G   Q   V   G   P   G   A     619
CGG CGG GGG CGG GCC ATG GCA GCA GCG GCT CAG GAC AAA GGG CAG GTG GGG CCA GGG GCT  2016

G   P   L   E   L   E   G   V   K   V   P   L   E   P   G   P   K   A   T   E     639
GGG CCC CTG GAA CTG GAG GGA GTG AAG GTC CCC TTG GAG CCA GGC CCG AAG GCA ACA GAG  2076

G   G   G   E   A   L   P   S   G   S   E   C   E   V   P   L   M   G   F   P     659
GGC GGT GGA GAG GCC CTG CCC AGC GGG TCT GAG TGT GAG GTG CCA CTC ATG GGC TTC CCA  2136

G   P   G   L   Q   S   P   L   H   A   K   P   Y   I   *                         674
GGG CCT GGC CTC CAG TCA CCC CTC CAC GCA AAG CCC TAC ATC TAA                      2181
```

FIG. 22D

GCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTA 2260

AGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCG 2339

GTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT 2418

CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGC 2497

TGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCG 2576

GCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTTAGGAACATGTTT 2655

TGCTTTTTTAAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACTCAGAGAC 2734

AAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAAATAAAAGATGAAGTGTGAAAAAA 2813

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2852

FIG. 22E

```
                1                                                           60
LRSG-1    MCSRVPLLLPLLLLL---ALGP-GVQG-------------CPSGCQCS-----QPQTVFC
GPV       M-LRGTLLCAVLGLLR-------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP     MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

                61                                                         120
LRSG-1    TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
GPV       SGGDVARISALGLP------------------------TNLTHILLFGMGRGVLQSQSFS
IGFBP     SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

                121                                                        180
LRSG-1    PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
GPV       GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP     GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

                181                                                        240
LRSG-1    NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
GPV       NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP     NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

                241                                                        300
LRSG-1    RLRNLHDLDVSDNQLERVPP-VIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
GPV       AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP     QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS

                301                                                        360
LRSG-1    NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP
GPV       RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWL-----NRTQL--
IGFBP     HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTL-----DHNQLQE
```

FIG. 23A

```
          361                                                           420
LRSG-1    KNAGRLL--LELDYADFG--CPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTA-PAT
GPV       ----------------------RTLPAAAFRNLSRLRYLGVTLSPRLSA--LPQGAFQGL
IGFBP     VKVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLE-GSCLGR--IRPHTFAGL

          421                   *    *     *            * *        *480
LRSG-1    EAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLG---TRHHLACLCPEGFTGLYCES-
GPV       GELQVLALHSNGLTALPDGL-------LRGLGKLRQVSLRRNRLRALPRALFRNLSSLES
IGFBP     SGLRRLFLKDNGLVGIEEQS-------LWGLAELLELDLTSNQLTHLPHQLFQGLGKLEY

          481                                                           540
LRSG-1    -QMGQGTRPS-PTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNL
GPV       VQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCDCG-LGPFLG-------WLR-QHLGL
IGFBP     LLLSHNRLAELPADALGPLQRAFWLDVSHNRLEALPGSLLASLG-------RLR--YLNL

          541                                                           600
LRSG-1    SGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHS
GPV       VGGEEPPRCAG-PGAHAGLPLWALPGGD--AECPGPRGPPPRPAADSSSEAPVHPALAPN
IGFBP     R--NNSLRTFT-PQPPGLERLW-LEGNP--WDCSCPLKALRDFALQNPSAVPR-------

          601                                                           660
LRSG-1    NHAP------VTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV
GPV       SSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIK--------------
IGFBP     ------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL-------------------

          661                                                        718
LRSG-1    GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
GPV       ---IGQLFRKLIRER-ALG---------------------------------------
IGFBP     --------RDLGEAHFAPC---------------------------------------
```

FIG. 23B

```
GTCGACCCACGCGTCCGGGAGCCGGAGCCAGAGACCGGGGCTGGGAAACCCCAGCCCGGGACGGGACGCAGCAGCCTCT  79

GGATCCCGGGACCCCGGACCTCTCAGGACCGGCCAGAGGTGAAGGACTGAGGCCCCACTGAGGCCTTGGACCGCACCGC  158

                                     M   H   S   R   S   C   L   P   P   L       10
CTGGCTCCTTCAGCCGCAGTCGTCTCCTGGGACAGAAG ATG CAC TCC AGG AGC TGC CTG CCA CCT CTC  226

 L   L   L   L   L   V   L   L   G   S   G   V   Q   G   C   P   S   G   C   Q     30
CTG TTG TTG CTT CTG GTG CTC CTG GGG TCT GGA GTA CAG GGT TGC CCA TCA GGC TGC CAG   286

 C   N   Q   P   Q   T   V   F   C   T   A   R   Q   G   T   T   V   P   R   D     50
TGC AAC CAG CCA CAG ACA GTC TTC TGC ACT GCC CGT CAG GGA ACC ACA GTG CCC CGA GAC   346

 V   P   P   D   T   V   G   L   Y   I   F   E   N   G   I   T   T   L   D   V     70
GTG CCA CCT GAC ACA GTG GGC CTG TAC ATC TTT GAG AAC GGC ATC ACG ACA CTT GAT GTG   406

 G   C   F   A   G   L   P   G   L   Q   L   L   D   L   S   Q   N   Q   I   T     90
GGC TGT TTT GCT GGC CTT CCG GGC CTG CAG CTT CTG GAC TTG TCA CAG AAC CAG ATC ACT   466

 S   L   P   G   G   I   F   Q   P   L   V   N   L   S   N   L   D   L   T   A    110
AGC CTG CCC GGG GGC ATC TTT CAG CCA CTT GTT AAC CTC AGT AAC CTG GAC CTG ACT GCC   526

 N   K   L   H   E   I   S   N   E   T   F   R   G   L   R   R   L   E   R   L    130
AAC AAA CTG CAC GAG ATC TCC AAC GAG ACC TTC CGT GGC CTG CGG CGC CTG GAG CGC CTC   586

 Y   L   G   K   N   R   I   R   H   I   Q   P   G   A   F   D   A   L   D   R    150
TAC CTG GGC AAG AAC CGA ATT CGC CAC ATC CAA CCG GGT GCC TTC GAC GCG CTT GAT CGC   646
```

FIG. 24A

```
L   L   E   L   K   L   P   D   N   E   L   R   V   L   P   P   L   H   L   P    170
CTC CTG GAG CTC AAG CTG CCA GAC AAT GAG CTT CGG GTG TTG CCC CCA TTG CAC TTG CCC  706

R   L   L   L   L   D   L   S   H   N   S   I   P   A   L   E   A   G   I   L    190
CGC CTG CTG CTG CTT GAC CTC AGC CAC AAC AGC ATC CCA GCC CTG GAA GCC GGA ATA CTG  766

D   T   A   N   V   E   A   L   R   L   A   G   L   G   L   R   Q   L   D   E    210
GAT ACC GCC AAT GTA GAG GCA TTG AGG TTG GCT GGC CTA GGG CTG CGG CAG CTG GAT GAG  826

G   L   F   G   R   L   L   N   L   H   D   L   D   V   S   D   N   Q   L   E    230
GGG CTT TTT GGC CGC CTT CTC AAC CTC CAT GAC TTG GAT GTT TCT GAC AAC CAG TTG GAG  886

H   M   P   S   V   I   Q   G   L   R   G   L   T   R   L   R   L   A   G   N    250
CAT ATG CCA TCT GTG ATT CAA GGC CTG CGT GGC CTG ACA CGC CTG CGG CTG GCT GGC AAC  946

T   R   I   A   Q   I   R   P   E   D   L   A   G   L   T   A   L   Q   E   L    270
ACC CGT ATT GCC CAG ATA CGG CCC GAG GAC CTC GCT GGT CTG ACT GCC CTA CAG GAA TTG  1006

D   V   S   N   L   S   L   Q   A   L   P   S   D   L   S   S   L   F   P   R    290
GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG CCC AGT GAC CTC TCG AGT CTC TTT CCC CGC  1066

L   R   L   L   A   A   A   R   N   P   F   N   C   L   C   P   L   S   W   F    310
CTG CGC CTC TTA GCA GCT GCC AGG AAC CCC TTC AAC TGC TTG TGC CCC TTG AGC TGG TTT  1126

G   P   W   V   R   E   N   H   V   V   L   A   S   P   E   E   T   R   C   H    330
GGT CCT TGG GTG CGT GAG AAC CAT GTT GTG TTG GCC AGC CCT GAG GAG ACG CGT TGT CAC  1186
```

FIG. 24B

```
 F   P   P   K   N   A   G   R   L   L   L   D   L   D   Y   A   D   F   G   C    350
TTT CCA CCC AAG AAT GCT GGC CGA CTG CTC CTG GAT CTG GAT TAT GCA GAT TTT GGC TGC  1246

 P   V   T   T   T   T   A   T   V   P   T   I   R   S   T   I   R   E   P   T    370
CCA GTC ACC ACT ACC ACG GCC ACA GTA CCT ACT ATA AGG TCT ACT ATC AGG GAA CCC ACA  1306

 L   S   T   S   S   Q   A   P   T   W   P   S   L   T   E   P   T   T   Q   A    390
CTT TCA ACT TCT AGC CAA GCT CCC ACC TGG CCC AGC CTC ACA GAG CCA ACT ACC CAG GCC  1366

 S   T   V   L   S   T   A   P   P   T   M   R   P   A   P   Q   P   Q   D   C    410
TCC ACC GTA CTA TCG ACT GCC CCA CCA ACC ATG AGG CCA GCT CCT CAG CCC CAG GAC TGT  1426

 P   A   S   I   C   L   N   G   G   S   C   R   L   G   A   R   H   H   W   E    430
CCA GCA TCC ATC TGC CTG AAT GGT GGT AGC TGC CGT TTG GGA GCA AGA CAC CAC TGG GAG  1486

 C   L   C   P   E   G   F   I   G   L   Y   C   E   S   P   V   E   Q   G   M    450
TGC CTA TGC CCT GAG GGC TTC ATT GGC CTG TAC TGT GAG AGT CCA GTG GAG CAA GGG ATG  1546

 K   P   S   S   I   P   D   T   P   R   P   P   P   L   L   P   L   S   I   E    470
AAG CCC AGC TCC ATA CCA GAC ACT CCA AGG CCC CCT CCA CTG CTG CCT CTC AGC ATT GAG  1606

 P   V   S   P   T   S   L   R   V   K   L   Q   R   Y   L   Q   G   N   T   V    490
CCG GTG AGC CCC ACC TCC TTG CGT GTG AAG CTG CAG CGC TAC TTG CAG GGT AAC ACT GTG  1666

 Q   L   R   S   L   R   L   T   Y   R   N   L   S   G   P   D   K   R   L   V    510
CAG CTA CGG AGC CTC CGG CTC ACC TAT CGC AAC CTG TCT GGC CCT GAC AAA CGA CTG GTG  1726
```

FIG. 24C

```
T   L   R   L   P   A   S   L   A   E   Y   T   V   T   Q   L   R   P   N   A    530
ACA TTA CGG CTG CCT GCT TCA CTT GCA GAG TAT ACA GTC ACC CAG CTG CGA CCC AAT GCC  1786

T   Y   S   I   C   V   T   P   L   G   A   G   R   T   P   E   G   E   E   A    550
ACC TAT TCT ATC TGT GTC ACA CCC TTG GGA GCT GGA CGG ACA CCT GAA GGT GAG GAG GCC  1846

C   G   E   A   N   T   S   Q   A   V   R   S   N   H   A   P   V   T   Q   A    570
TGT GGG GAG GCC AAC ACT TCC CAG GCA GTC CGC TCT AAC CAT GCC CCA GTT ACC CAG GCC  1906

R   E   G   N   L   P   L   L   I   A   P   A   L   A   A   V   L   L   A   V    590
CGT GAG GGC AAC CTG CCA CTC CTC ATT GCG CCT GCC CTG GCT GCT GTA CTT CTG GCT GTG  1966

L   A   A   A   G   A   A   Y   C   V   R   R   A   R   A   T   S   T   A   Q    610
TTA GCC GCT GCA GGG GCA GCC TAC TGT GTG CGG CGG GCA CGG GCA ACT TCT ACA GCT CAG  2026

D   K   G   Q   V   G   P   G   T   G   P   L   E   L   E   G   V   K   A   P    630
GAC AAA GGG CAG GTG GGG CCA GGG ACT GGA CCC CTG GAA CTA GAG GGG GTG AAA GCC CCT  2086

L   E   P   G   S   K   A   T   E   G   G   G   E   A   L   S   G   G   P   E    650
TTG GAG CCA GGC TCC AAG GCA ACA GAG GGA GGT GGG GAG GCT TTG TCA GGT GGT CCT GAA  2146

C   E   V   P   L   M   G   Y   P   G   P   S   L   Q   G   V   L   P   A   K    670
TGT GAG GTG CCT CTT ATG GGC TAC CCA GGG CCC AGC CTT CAG GGG GTC CTC CCT GCT AAG  2206

H   Y   I   *                                                                    674
CAC TAC ATT TAG                                                                  2218
```

FIG. 24D

ACTGGTGAGAAAGAGCAGCCAGGGGGTCAGGCTTTCAGTCACCACCCTCCTGCTGCCACAGAAGGAAGTTCTCAGTATA 2297

CACCACAGTGCACGTGCATGATGGAGCTGTGGGACCCTCTCTGGGCTGGGTCTCATCTGTAAGCTGCTACAGCCCAGAT 2376

GAACTCTGCCAGCCGCCAGTGCATCCAGTACAGCGCCTGCCATCTTGTGCAATGTGCAACCCTGGGATGTGAGCCCTGC 2455

CATGTGCTGGTAACATGGCTAGGCATGTTGGGCTTCCCAAACCATGGAGTCTGGTAACCAGTGAAGGAAGCCCCCAGAA 2534

ATAATGAGTGGGGAAGGTACTAGGGCACTGGCCTTGGCCTCAAAAGTGCAGGCACACTTGAAACTGGAAAGGAAGGTGC 2613

TCTGGGCACATGTGGATTTGCTTCTATTGTTTTGTTTTGTTTTTTCTAATGTATTTATAAAAGATCTTTTCCCATTTAT 2692

GCTGGGAAAGTGTTTTTCAAACTCAGTGACAAGGACTTTGGTTTTTGTAAGACTGTTGATGATATGAAGGCCTTTTGTA 2771

AGAAAATAAAAAATAAAGTAAAAAAAAAAAAAAAGGGCGGCCGC 2815

FIG. 24E

```
                 10        20        30        40        50
inputs MCSRVPLL-LPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYV
       : ::   :   : ::::. ::.::::::::::.::::::::::::::::::::::::::.
       MHSRSCLPPLLLLLLVLLGSGVQGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYI
               10        20        30        40        50        60

        60        70        80        90       100       110
inputs FENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNET
       :::::: ::.: ::::::::::::::::.:::.:.::::.::::::::::.::::.:::
       FENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNET
               70        80        90       100       110       120

       120       130       140       150       160       170
inputs FRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHN
       :::::::::::::::::::::::::.:::::::::.:::::.::::.:::::::::::::
       FRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHN
              130       140       150       160       170       180

       180       190       200       210       220       230
inputs SLLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLR
       :.  :::.:::::::::::::::::::.::::::::.:: ::::::::::::..:.::.:::
       SIPALEAGILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLDVSDNQLEHMPSVIQGLR
              190       200       210       220       230       240

       240       250       260       270       280       290
inputs GLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNP
       ::::::::::::::.::::::::.:::::::::::::::::.:::.::::::::::::::
       GLTRLRLAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNP
              250       260       270       280       290       300
```

FIG. 25A

```
       300       310       320       330       340       350
inputs FNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVP
       :::.:::::::::::.::.::::::::::::::::::::::.:::::::::.::::::::
       FNCLCPLSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLDLDYADFGCPVTTTTATVP
              310       320       330       340       350       360

       360       370       380       390       400       410
inputs TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGT
       :.:...::::  .:: :::: : :.:.:.:..  ::::::. :.:::::::.:.:::::.
       TIRSTIREPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGS
              370       380       390       400       410       420

       420       430       440       450       460       470
inputs CHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVG
       :.::.::: .:::::::.::::::.. :: .::..: :::::   : :.::::::::::
       CRLGARHHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPPLLPLSIEPVSPTSLRVK
              430       440       450       460       470       480

       480       490       500       510       520       530
inputs LQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLG
       :::::::..:::::::::::::::::::::::::::::::::::::::::::::.:: :::
       LQRYLQGNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLG
              490       500       510       520       530       540

       540       550       560       570       580       590
inputs PGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCV
       .::.:::::::::.:..::.::::::::::::::::::::::::::::.:::.::::::
       AGRTPEGEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCV
              550       560       570       580       590       600
```

FIG. 25B

```
        600       610       620       630       640       650
inputs RRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP
       ::.:: ...:::::::::.::::::::.:::::.::::::::::..:.::::::::.:
       RRARA-TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGEALSGGPECEVPLMGYP
                  610       620       630       640       650

        660       670
inputs GPGLQSPLHAKPYI
       ::.::. : :: ::
       GPSLQGVLPAKHYI
        660       670
```

FIG. 25C

```
                  1                                                          60
human LRSG-1      MCSR---VPLLLPLLLLLALGP-GVQG-------------CPSGCQCS-----QPQTVFC
murine LRSG-1     MHSRSC-LPPLL-LLLLVLLGS-GVQG-------------CPSGCQCN-----QPQTVFC
GPV               M-LRGTLLCAVLGLLR-------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP             MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

                  61                                                        120
human LRSG-1      TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
murine LRSG-1     TARQGTTVPR-DVPPDTVGLYIFENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQ
GPV               SGGDVARISALGLP------------------------TNLTHILLFGMGRGVLQSQSFS
IGFBP             SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

                  121                                                       180
human LRSG-1      PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
murine LRSG-1     PLVNLSNLDLTANKLHEISNETFRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPD
GPV               GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP             GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

                  181                                                       240
human LRSG-1      NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
murine LRSG-1     NELRVLPPLHLPRLLLLD---LSHNSIPALEAGILDT-ANVEALRLAGLGLRQLDEGLFG
GPV               NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP             NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

                  241                                                       300
human LRSG-1      RLRNLHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
murine LRSG-1     RLLNLHDLDVSDNQLEHM-PSVIQGLRGLTRLRLAGNTRIAQIRPEDLAGLTALQELDVS
GPV               AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP             QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS
```

FIG. 26A

```
                301                                                          360
human LRSG-1    NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP
murine LRSG-1   NLSLQALPSDLSSLFPRLRLLAAARNPFNCLCPLSWFGPWVRENHVVLASPEETRCHFPP
GPV             RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWLNRTQ--------
IGFBP           HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTLDHNQ--------

                361                                                          420
human LRSG-1    KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP
murine LRSG-1   KNAGRLLLDLDYADFGCPVTTTTATVPTIRSTIREPTLSTSSQAPTWPSLTEPTTQASTV
GPV             ------L-------------------------RT--------------LPAAAFRNLSR
IGFBP           ------LQEVKVGAF--LGLTNVAVMNLSGNCLRN--------------LPEQVFRGLGK

                421                *   *    *       * *     *              480
human LRSG-1    PSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPS
murine LRSG-1   LSTAPPTMRPAPQPQDCPASICLNGGSCRLGARHHWECLCPEGFIGLYCESPVEQGMKPS
GPV             LRYLGVTLSP-----------------RLSA------LPQGAFQGL-------------
IGFBP           LHSLHLE-GS-----------------CLGR------IRPHTFAGL-------------

                481                                                          540
human LRSG-1    PTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGS--SVQLRSL-RLTYRNLSGPDKRLV
murine LRSG-1   SIPDTPRPPPLLPLSIEPVSPTSLRVKLQRYLQGN--TVQLRSL-RLTYRNLSGPDKRLV
GPV             ---GELQVLALHSNGLTALPDGLLR-GLGKLRQVSLRRNRLRALPRALFRNLSSLESVQL
IGFBP           ---SGLRRLFLKDNGLVGIEEQSLW-GLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLL

                541                                                          600
human LRSG-1    TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQA
murine LRSG-1   TLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPEGEEACGEANTSQAVRSNHAPVTQA
GPV             DHNQLETLPGDVFGALPRLTEVLLGHNSW--------RCDCG-LGPFLGWLRQHLGL---
IGFBP           SHNRLAELPADALGPLQRAFWLDVSHNRL--------EALPGSLLASLGRLR-YLNL---
```

FIG. 26B

```
                601                                                         660
human LRSG-1    REGNLPLLIAPALAAVLLAALAAVGAAY-CVRRGRAMAAAAQDKGQVGPGAGPLELEGVK
murine LRSG-1   REGNLPLLIAPALAAVLLAVLAAAGAAY-CVRRARA-TSTAQDKGQVGPGTGPLELEGVK
GPV             VGGEEPPRCAGPGAHAGLPLWALPGGDAECPGPRGPPPRPAADSSSEAP---------VH
IGFBP           R--NNSLRTFTPQPPGLERLW-LEGNPWDCSCPLKALRDFALQNPSAVP---------R-

                661                                                         720
human LRSG-1    VPLEPGPKATEGGGEALPSGS-ECEVPLMGF-----PGPGLQSP---------------L
murine LRSG-1   APLEPGSKATEGGGEALSGGP-ECEVPLMGY-----PGPSLQGV---------------L
GPV             PALAPNSSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIKIGQLFRKL
IGFBP           ------------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL----------RDL

                721    728
human LRSG-1    HAKPYI--
murine LRSG-1   PAKHYI--
GPV             IRER-ALG
IGFBP           GEAHFAPC
```

FIG. 26C

```
GAATTCCCGGGTCGACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGCTGAGCGAAGCGCGGCGGCGGCGGCGG  79

CGCCTAGGGGAGGGAGGGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCGCCAGCATGC  158

CCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGCGCGGGAACC  237

GCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCCCCAGCATCC  316

TTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGCCAGCTCCGG  395

          M   S   D   E   R   R   L   P   G   S   A   V   G   W   L   V   C       17
TCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG GTA TGT     454

 G   G   L   S   L   L   A   N   A   W   G   I   L   S   V   G   A   K   Q   K    37
GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG CAG AAG  514

 K   W   K   P   L   E   F   L   L   C   T   L   A   A   T   H   M   L   N   V    57
AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA AAT GTG  574

 A   V   P   I   A   T   Y   S   V   V   Q   L   R   R   Q   R   P   D   F   E    77
GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC TTC GAG  634

 W   N   E   G   L   C   K   V   F   V   S   T   F   Y   T   L   T   L   A   T    97
TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG GCC ACC  694

 C   F   S   V   T   S   L   S   Y   H   R   M   W   M   V   C   W   P   V   N   117
TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT GTC AAC  754

 Y   R   L   S   N   A   K   K   Q   A   V   H   T   V   M   G   I   W   M   V   137
TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG ATG GTG  814

 S   F   I   L   S   A   L   P   A   V   G   W   H   D   T   S   E   R   F   Y   157
TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC TTC TAC  874

 T   H   G   C   R   F   I   V   A   E   I   G   L   G   F   G   V   C   F   L   177
ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC TTC CTG  934

 L   L   V   G   G   S   V   A   M   G   V   I   C   T   A   I   A   L   F   Q   197
CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC TTC CAG  994

 T   L   A   V   Q   V   G   R   Q   A   D   H   R   A   F   T   V   P   T   I   217
ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC ACC ATC  1054

 V   V   E   D   A   Q   G   K   R   R   S   S   I   D   G   S   E   P   A   K   237
GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC GCC AAA  1114

 T   S   L   Q   T   T   G   L   V   T   T   I   V   F   I   Y   D   C   L   M   257
ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC CTC ATG  1174

 G   F   P   V   L   D   S   T   P   I   P   E   R   S   A   V   R   Q   G   E   277
GGC TTC CCT GTG CTG GAC TCT ACG CCC ATC CCC GAA AGG TCT GCA GTG AGA CAG GGA GAG  1234

 D   W   G   K   D   Q   P   E   G   F   H   P   S   S   R   Q   D   C   L   P   297
GAC TGG GGC AAA GAC CAG CCT GAG GGG TTT CAT CCA AGC AGC AGG CAA GAC TGC CTT CCC  1294

 *                                                                               298
TGA                                                                             1297
```

Fig. 27A

GCCATTGCAGGACATGAGGACATGAGCTCCAGAATGGTGCCAGGCCGAGCCCTGTGCCCACAGGTGGTGAGCTTCAGCA 1376
GCCTGCGGGCCGACGCCTCAGCGCCCTGGATGGCACTCTGCGTGCTGTGGTGCTCCGTGGCCCAGGCCCTGCTTCCGAC 1455
CTGTCCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTG 1534
TAGGCCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAG 1613
CATGTGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCA 1692
CCCCAGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCA 1771
TTACTCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGG 1850
AGAGCACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGG 1929
CCAGGAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGC 2008
AATGTATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGTCTTCCCAGGC 2087
TAAGGAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTAC 2166
CCCTACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTT 2245
CTGGCCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGG 2324
TGGGAGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGT 2403
GGCCACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGC 2482
CTTCAAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCA 2561
CTTGTCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCA 2640
GGGGGACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTG 2719
GGCCTGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAG 2798
CACACCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTT 2877
CCTTATGATTTGCAAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig 27B

GAATTCCCGGGTCGACCCACGCGTCCGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCG 79

CCAGCATGCCCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGC 158

GCGGGAACCGCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCC 237

CCAGCATCCTTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGC 316

M S D E R R L P G S A V G W L 15

CAGCTCCGGTCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG 378

V C G G L S L L A N A W G I L S V G A K 35

GTA TGT GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG 438

Q K K W K P L E F L L C T L A A T H M L 55

CAG AAG AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA 498

N V A V P I A T Y S V V Q L R R Q R P D 75

AAT GTG GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC 558

F E W N E G L C K V F V S T F Y T L T L 95

TTC GAG TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG 618

A T C F S V T S L S Y H R M W M V C W P 115

GCC ACC TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT 678

V N Y R L S N A K K Q A V H T V M G I W 135

GTC AAC TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG 738

M V S F I L S A L P A V G W H D T S E R 155

ATG GTG TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC 798

F Y T H G C R F I V A E I G L G F G V C 175

TTC TAC ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC 858

F L L L V G G S V A M G V I C T A I A L 195

TTC CTG CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC 918

F Q T L A V Q V G R Q A D H R A F T V P 215

TTC CAG ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC 978

T I V V E D A Q G K R R S S I D G S E P 235

ACC ATC GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC 1038

A K T S L Q T T G L V T T I V F I Y D C 255

GCC AAA ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC 1098

L M G F P V L V V S F S S L R A D A S A 275

CTC ATG GGC TTC CCT GTG CTG GTG GTG AGC TTC AGC AGC CTG CGG GCC GAC GCC TCA GCG 1158

P W M A L C V L W C S V A Q A L L L P V 295

CCC TGG ATG GCA CTC TGC GTG CTG TGG TGC TCC GTG GCC CAG GCC CTG CTG CTG CCT GTG 1218

F L W A C D R Y R A D L K A V R E K C M 315

TTC CTC TGG GCC TGC GAC CGC TAC CGG GCT GAC CTC AAA GCT GTC CGG GAG AAG TGC ATG 1278

A L M A N D E E S D D E T S L E G G I S 335

GCC CTC ATG GCC AAC GAC GAG GAG TCA GAC GAT GAG ACC AGC CTG GAA GGT GGC ATC TCC 1338

Fig. 28A

P D L V L E R S L D Y G Y G G D F V A L 355
CCG GAC CTG GTG TTG GAG CGC TCC CTG GAC TAT GGC TAT GGA GGT GAT TTT GTG GCC CTA 1398

D R M A K Y E I S A L E G G L P Q L Y P 375
GAT AGG ATG GCC AAG TAT GAG ATC TCC GCC CTG GAG GGG GGC CTG CCC CAG CTC TAC CCA 1458

L R P L Q E D K M Q Y L Q V P P T R R F 395
CTG CGG CCC TTG CAG GAG GAC AAG ATG CAA TAC CTG CAG GTC CCG CCC ACG CGG CGC TTC 1518

S H D D A D V W A A V P L P A F L P R W 415
TCC CAC GAC GAT GCG GAC GTG TGG GCC GCC GTC CCG CTG CCC GCC TTC CTG CCG CGC TGG 1578

G S G E D L A A L A H L V L P A G P E R 435
GGC TCC GGC GAG GAC CTG GCC GCC CTG GCG CAC CTG GTG CTG CCT GCC GGG CCC GAG CGG 1638

R R A S L L A F A E D A P P S R A R R R 455
CGC CGC GCC AGC CTC CTG GCC TTC GCG GAG GAC GCA CCA CCG TCC CGC GCG CGC CGC CGC 1698

S A E S L L S L R T S A L D S G P R G A 475
TCG GCC GAG AGC CTG CTG TCG CTG CGG ACC TCG GCC CTG GAT AGC GGC CCG CGG GGA GCC 1758

R D S P P G S P R R R P G P G P R S A S 495
CGC GAC TCG CCC CCC GGC AGC CCG CGC CGC CGC CCC GGG CCC GGC CCC CGC TCC GCC TCG 1818

A S L L P D A F A L T A F E C E P Q A L 515
GCC TCG CTG CTG CCC GAC GCC TTC GCC CTG ACC GCC TTC GAG TGC GAG CCA CAG GCC CTG 1878

R R P P G P F P A A P A A P D G A D P G 535
CGC CGC CCG CCC GGG CCC TTC CCC GCT GCG CCC GCC GCC CCC GAC GGC GCA GAT CCC GGA 1938

E A P T P P S S A Q R S P G P R P S A H 555
GAG GCC CCG ACG CCC CCA AGC AGC GCC CAG CGG AGC CCA GGG CCA CGC CCC TCT GCG CAC 1998

S H A G S L R P G L S A S W G E P G G L 575
TCG CAC GCC GGC TCT CTG CGC CCC GGC CTG AGC GCG TCG TGG GGC GAG CCC GGG GGG CTG 2058

R A A G G G G S T S S F L S S P S E S S 595
CGC GCG GCG GGC GGC GGC GGC AGC ACC AGC AGC TTC CTG AGT TCC CCC TCC GAG TCC TCG 2118

G Y A T L H S D S L G S A S * 610
GGC TAC GCC ACG CTG CAC TCG GAC TCG CTG GGC TCC GCG TCC TAG 2163

GACCGCCGGCGCCTCCCCACGGACGCCAGGCAGGCCAGGCCGCTCTCCGGGGCCGCAGCACCAAAGACGCCCGCCTCCC 2242

CCCCGCGCGCAGACATGCGCCACCCCTCCCAGGGGTGAGGGGGCGTTGGCCTCAGCGTTTGTCTTCCGGCTCCTCCCAG 2321

CTGGCCTTGTCCCAGGGGCGACGGCTGCCCCGGACGACTGCGCTGGGCACCGCATGTCCCGGGCCGAGTGAGGTCGGGC 2400

CTGGGGAGCTGAGTGACATCCCAAGCTTGGGCTTGGGTAGTGAGTGACATGTGCACACGTCCAGCTGCGCCATCACCAG 2479

CCCTGCGCAACAGGACGTCGGGAGCAGGGAACCTGAGACAGGGCCACTGCGGGATCGGACAAAGCCCCGCTTTGGAGAG 2558

GCTGAGCTGGAGCCATTGGCCTCCCCAGGGGCTTTCCACCCACACTGCACCATAACCGCCACACCCTTCGGGGGGGGGG 2637

AGGGTACAGAGGGTCTCTAAGCACAGGGGTGTTCAGAGCCCGAACAAGCTTTGATCAGGTTTCCCTGCTTCCGACCTGT 2716

CCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTGTAGG 2795

Fig. 28B

CCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAGCATG 2874

TGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCACCCC 2953

AGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCATTAC 3032

TCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGGAGAG 3111

CACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGGCCAG 3190

GAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGCAATG 3269

TATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGGTCTTCCCAGGCTAAG 3348

GAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTACCCCT 3427

ACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTTCTGG 3506

CCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGGTGGG 3585

AGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGTGGCC 3664

ACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGCCTTC 3743

AAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCACTTG 3822

TCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCAGGGG 3901

GACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTGGGCC 3980

TGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAGCACA 4059

CCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTTCCTT 4138

ATGAAAAAAAAAAAAAAAAGGGCGGCCGC 4166

Fig. 28C

```
            1                                                          60
SSTM-1      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
SSTM-2      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
proteinA-2  MARGGAGAEEASLRSNALSWLACGLLALLANAWIILSISAKQQKHKPLELLLCFLAGTHI
proteinA-3  ------------------------------------------------------------

            61                                                        120
SSTM-1      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
SSTM-2      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
proteinA-2  LMAAVPLTTFAVVQLRRQASSDYDWNESICKVFVSTYYTLALATCFTVASLSYHRMWMVR
proteinA-3  ------------------------------------------------------------

            121                                                       180
SSTM-1      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
SSTM-2      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
proteinA-2  WPVNYRLSNAKKQALHAVMGIWMVSFILSTLPSIGWHNNGERYYARGCQFIVSKIGLGFG
proteinA-3  ------------------------------------------------------------

            181                                                       240
SSTM-1      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
SSTM-2      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
proteinA-2  VCFSLLLLGGIVMGLVCVAITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE
proteinA-3  ------------------ITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE

            241                                                       300
SSTM-1      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL-----------
SSTM-2      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVLVVSFSSLRADA
proteinA-2  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLVSAIVFLYDSLTGVPILVVSFFSLKSDS
proteinA-3  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLV-----------------VSFFSLKSDS

            301                                                       360
SSTM-1      ------------------------------------------------------DSTPI---
SSTM-2      SAPWMALCVLWCSVAQALLLPVFLWACDRYRADLKAVREKCMALMANDEESDDETSLEGG
proteinA-2  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G
proteinA-3  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G

            361                                                       420
SSTM-1      -----------------------------------------------------------P
SSTM-2      ISPDLVLER--SLDYGYGGDFVALDRMAKYEISALEGGLPQLYPLRPLQEDKMQYLQVPP
proteinA-2  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQVPL
proteinA-3  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQLK-

            421                                                       480
SSTM-1      ERSAVRQGED-------------WGKDQ--------------------------------
SSTM-2      TRRFSHDDADVWAAVPLPA-FLPRWGSGEDLAALAHLVLP-AGPERRRASLLAFAEDAPP
proteinA-2  SRRLSHDETNIFSTPREPGSFLHKWSSSDDIRVLPAQSRALGGPPEYLGQRHRLEDEEDE
proteinA-3  KLDLAAAAAHTF----------------------------------FVANPMHLQ-----

            481                                                       540
SSTM-1      -----------------------------------------------------PEGFH-----
SSTM-2      SRARRRSAESLLSLRTSALDSGPRGARDSPPGSPRRRPGPGPRSASASLLPDAFALTAFE
proteinA-2  EEA---EGGGLASLRQF-LESGVLGSGGGPP------RGPG-------FFRE--EITTF-
proteinA-3  ---------------------------------------------MRE--DMAKY-
```

Fig. 29A

```
              541                                                        600
SSTM-1        --------------------------------------PSSRQ-----------------
SSTM-2        CEPQALRRPPGPFPAAPAAPDGADPGEAPTPPSSAQRSPGPRP--SAHSHAGSLRPGLSA
proteinA-2    ------------IDETPLPSPTASPGHSPRRPRPLGLSPRRLSLGSPESRAVGLPLGLSA
proteinA-3    ---------------------------------------RRMS-----------------

              601                                      642
SSTM-1        -----------------------------------DCL---P
SSTM-2        SWGEPGGLRAAGGGGSTSSFLSSPSESSGYATLHSDSLGSAS
proteinA-2    ------GRRCSLTGGEESARAWGGSWGPGNPIFPQLTL----
proteinA-3    ------GVR---------------------------------
```

Fig. 29B

Fig. 30A

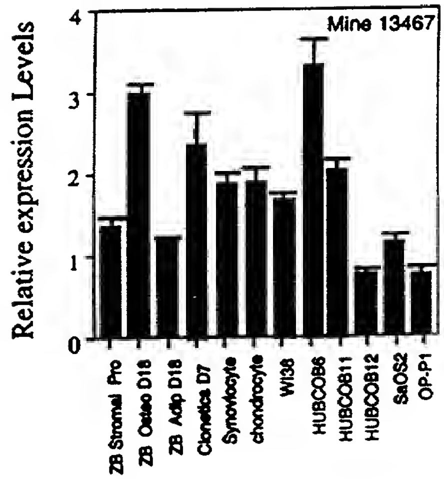


Fig. 30B

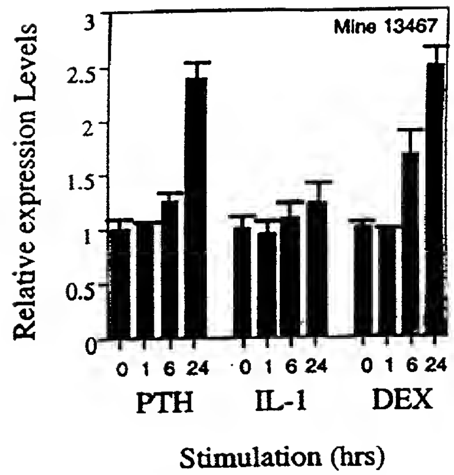
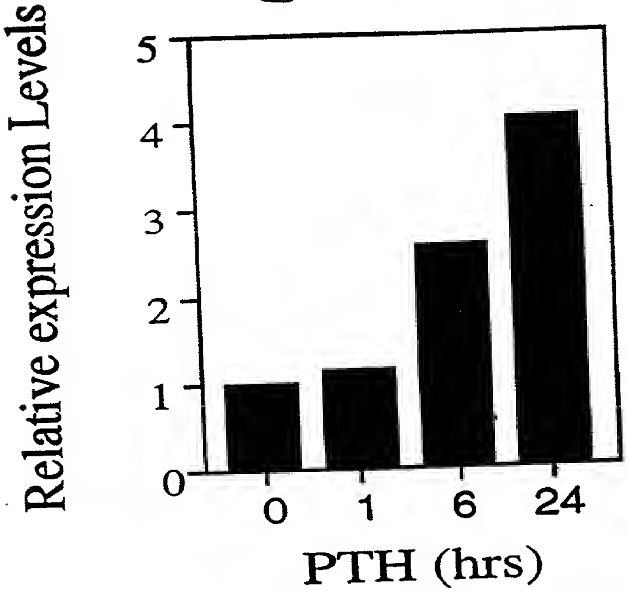


Fig. 30C



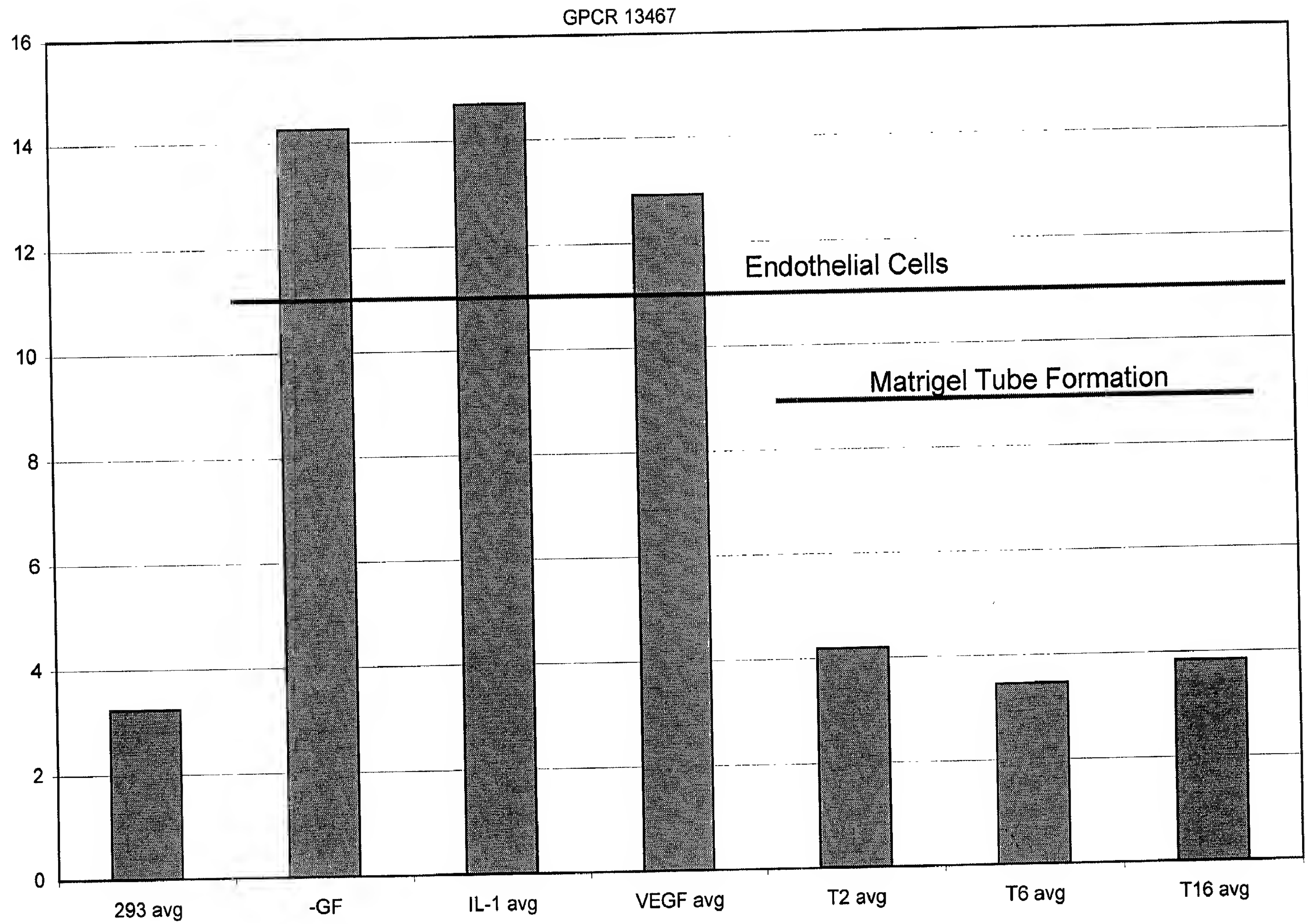

GPCR 13467
16
14
12
10
8
6
4
2
0
Endothelial Cells
Matrigel Tube Formation
293 avg
-GF
IL-1 avg
VEGF avg
T2 avg
T6 avg
T16 avg

Fig. 31